
Dec 10 06:47

US-08-446-915-2.rsp

(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 10 07:03:26 1996; MasPar time 11.71 Seconds 607.114 Million cell updates/sec

Tabular output not generated.

Run on:

>US-08-446-915-2 (1-409) from US08446915.pep 2945

Description: Perfect Score:

Sequence: 1 MASSSAPDENEFQFGCPPAP......KHAYVKDDTMF1KCIVDTSA 409

Scoring table: PAM 150 Gap 11

49340 seqs, 17385503 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 49.616; Variance 101.312; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
<u>, , , , , , , , , , , , , , , , , , , </u>	2945	100.0	409	8	TRF1 MOUSE	TNF RECEPTOR ASSOCIAT	0.00e+00
2	972	33.0	501	8	TRF2 MOUSE	TNF RECEPTOR ASSOCIAT	3.50e-163
w	148	5.0	760	5	MEPA MOUSE	MEPRIN A ALPHA-SUBUNI	7.90e-07
4	127	4.3	1048	-	SBCC ECOLI	EXONUCLEASE SBCC.	7.06e-04
5	120	4.1	2291	٦	SPCB DROME	SPECTRIN BETA CHAIN.	6.00e-03
5	115	3.9	1319	w	DY15 DROME	150 KD DYNEIN-ASSOCIA	2.65e-02
7	112	3.8	493	4	INVO SAGOE	INVOLUCRIN.	6.32e-02
∞	112	3.8	870	σ	POL JSRV	POL POLYPROTEIN (REVE	6.32e-02
9	113	3.8	1427	~1	REST HUMAN	RESTIN (CYTOPLASMIC L	4.74e-02
10	109	3.7	544	4	INVO AOTTR	INVOLUCRIN.	1.49e-01
1	106	3.6	668	5	MEPB RAT	MEPRIN A BETA-SUBUNIT	3.44e-01
12	105	3.6	776	_	ARCB ECOLI	AEROBIC RESPIRATION C	4.53e-01
13	107	3.6	2663	2	CENE_HUMAN	CENTROMERIC PROTEIN E	2.61e-01

ALI GNMENTS

32 ED XO	SQ	Š	DR	റ്റ	CC	CC	ရှိ	æ	RA.	RX	RP	RN	င္ပ	8	SO	DΕ	DT	ΡŢ	DT	AC	ID	RES
Query Match 100.0%; Score 2945; DB 8; Length 409; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 409 AA; 45464 MW; 857796 CN;	COILED COIL.	EMBL; 135302; 135302.	-!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.	OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).		CELL /8:681-692(1994).	ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;	MEDLINE; 94349371.	SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.	[1]	EUTHERIA; RODENTIA.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	MUS MUSCULUS (MOUSE).	TNF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1).	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)	01-FEB-1995 (REL. 31, CREATED)	P39428;	TRF1 MOUSE STANDARD; PRT; 409 AA.	RESULT 1

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                                                                                                    Query Match
Best Local Similarity
                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   TRF2 MOUSE
P39429;
01-FEB-1995
                                                                                                                                                                                                    -!- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TW. -!- SUBCELLULAR LOCATION: CYTOPLASMIC. -!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2. -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                        ZN FING
                                                                                                                                                                 ZINC-FINGER; COILED COIL.
                                                                                                                                                                                                                                                                       MEDLINE; 94349371.

ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;

CELL 78:681-692(1994).
                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
                                                                                                                                                                            PROSITE; PS00518; ZINC_FINGER_C3HC4.
                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                         EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                               TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2)
                                                                                                                                           SEQUENCE
                                                                275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sspgsnlgsapmalernlselqlqaaveatgdlevdcyrapccesqeelalqhlvkekll
            madleqkvselevstydgvfiwkisdftrkrqeavagrtpaifspafytsrygykmclrv
                                     LEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVDTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQLEEKLRVFANI VAVLNKEVEASHLALAAS I HQSQLDREHLLS LEQRVVELQQTLAQKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSPGSNLGSAPMALERNLSELQLQAAVEATGDLEVDCYRAPCCESQEELALQHLVKEKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGSPLTQEKVHSDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pgspltqekvhsdvaeaeimcpfagvgcsfkgspqsmqeheatsqsshlylllavlkewk
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                                                                                                                                                                                             L35303; L35303.
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501 AA;
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(REL. 31, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
                                                                                        Conservative
                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                33.0%;
54.0%;
                                                                                                                                          56026 MW; 1264825
                                                                                    Score 972; DB 8; Le
Pred. No. 3.50e-163;
61; Mismatches 41;
                                                    ::
                                                                                                                                                       C3HC4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                  501
                                                                                                                                          2
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                                                                                        41;
                                                                                                                Length 501;
                                                                                                                                                                                                                                              (TNF-R2)
                                                                                                                                                                                                                                                            THE CYTOPLASMIC
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
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                                                                                                      EMBL; M74897; M74897.
EMBL; M82962; M82962.
PIR; A40195; A40195.
PDB; 11AF; 31-AUG-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEPA MOUSE
P28825;
01-DEC-1992
                                                                                                                                                                                                           METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY
-!- SIMILARITY: THE PROTEIN INCLUDES 1 EGF-LIKE REPEAT.
-!- SIMILARITY: CONTAINS A MAM DOMAIN.
                                                                                                                                                                                                                                                                                         SALIVARY DUCTS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAM.
OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NON-COVALENT
ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS; GENETIC FAC
DETERMINE WHICH OLIGOMER(S) WILL BE FORMED (STRAIN-SPECIFIC).
-!- PTM: N-GLYCOSYLATED; AT LEAST 3 OF THE POTENTIAL SITES ARE US!
-!- TISSUE SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOCHEMISTRY 30:8488-8493(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91355206.
WOLZ R.L., HARRIS R.B., BOND J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DUMERMUTH E., STERCHI E.E., JIANG W., FLANNERY A.V., BEYNON R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
ZYMOGEN; SIGNAL; EGF-LIKE DOMAIN;
                         HYDROLASE; METALLOPROTEASE; ZINC;
                                                  PROSITE; PS00142; ZINC PROTEASE. PROSITE; PS00740; MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTER IZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 77-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOND J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JIANG W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92250517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEP-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREFERENTIALLY ON CARBOXYL SIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
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24,
32,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
GLYCOPROTEIN;
3D-STRUCTURE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 R.J.,
                           TRANSMEMBRANE,
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SEQUENCE OF 378-1048 FROM N.A. MEDLINE; 92078081. REEDER T., SCHLEIF R.; J. BACTERIOL. 173:7765-7771(1991).
                                                                                           STRAIN=K12;
MEDLINE; 90045931.
NAOM I.S., MORTON S.J., LEACH D.R.F., LLOYD R.G.;
NUCLEIC ACIDS RES. 17:8033-8046(1989).
                                                                                                                                                                                                     ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 5.0%;
l Similarity 32.9%;
28; Conservative
                                                                                                                                                                                                                                                                           (REL. 13, CREATED)
(REL. 13, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
SBCC.
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CATALYTIC (ASTACIN DOMAIN).
MAM.
EGF-LIKE.
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EXTRACELLULAR (POTENTIAL).
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	RYTHROCYTE PLASMA MEMBRANE. HT: NATIVE SPECTRIN MOLECULE IS A TETRAMER (នន
ASSOCIATES TRUCTURE OF	NETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIAT WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE	88
	THE MAJOR CONSTITUENT OF THE CYTC	8
	ZHANG P., TALLURI S., DENG H., BRANTON D., WAGNER G.;	2 2
	UCTURE BY NMR OF 2145-2262.	굕
	ACAD. SCI. U.S.A. 8	2 E
	T.J., BRANDIN E., LUE R., WINOGR	R.
	SEQUENCE FROM N.A.	2 2
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	GOLDSTEIN L.S.;	9 ₹
	BYERS T.J., HUSAIN-CHISHTI A., DUBREUIL R.R., BRANTON D.,	₽:
	SEQUENCE OF 1-800 FROM N.A.	P P
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	DROSOPHILA MELANOGASTER (FRUIT FLY).	ဗ ဗ
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	(REL. 25, CREATED)	7
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		٠.
Gaps 4;	Query Match 4.3%; Score 127; DB 7; Length 1048; Best Local Similarity 34.7%; Pred. No. 7.06e-04; Matches 26; Conservative 14; Mismatches 31; Indels 4;	Z m 0
	SEQUENCE 1048 AA; 118721 MW; 4953805 CN;	SS
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	HYDROLASE; NUCLEASE; ATP-BINDING; COILED COIL.	골 등
	527548;	DR.
	PIR; JS0350; BVECSC.	R 5
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	-!- SIMILARITY: CONTAINS A COILED COIL MYOSIN-LIKE STRUCTURE.	88
AND TO	: TO PHAGE T4 GENE 46 PROTEIN AND PHAGE T5 D13	3 8
Of THE	CBCD ENZYME.	នន
	DNA PALINDROMES IN E.COLI. SBCC MAY HAVE A NUCLEASE ACTIVITY	3 8
OF	-!- FUNCTION: AFFECTS GENETIC RECOMBINATION AND THE VIABILITY OF	8 2
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	CHARACTERIZATION. MEDLINE; 93146416.	æ æ
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                                                           -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LOW MASS POLYPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DY15
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PROC. NATL. ACAD. SCI. U.S.A. 84:6501-6505(1987).
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-!- SIMILARITY: CONTAINS A CAP-GLY DOMAIN.
-!- SIMILARITY: STRONG, TO VERTEBRATE DYNACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN) .
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 KD DYNEIN-ASSOCIATED POLYPEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT AND THE N-TERMINUS OF THE BETA SUBUNIT.
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Similarity 27.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
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PS00020; ACTININ_2.
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(REL. 30, LAST ANNOTATION UPDATE)
N-ASSOCIATED POLYPEPTIDE (DP-150)
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                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.9%;
Best Local Similarity 25.0%;
                                                     Matches
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992
01-MAR-1992
01-DEC-1992
                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLYBASE; FBGN0001108; GL. PROSITE; PS00845; CAP_GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J02932; J02932.
PIR; A28313; A28313.
                                                                                                                                                                      -i- function: involucrin is a Keratinocyte protein that first appears in the cell cytosol, but ultimately becomes cross-linked to membrane proteins by transclutaminase. All that results in the formation of an insoluble envelope beneath the plasma membrane.
-i- tissue specificity: present in Keratinocytes of epidermis and
                                                                                                                                                                                                                                                                    MEDLINE; 92114750.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                 SAGUINUS OEDIPUS (COTTON-TOP TAMARIN)
                                                                                                                                                                                                                                                                                                                                                                                                                P24712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                        SEQUENCE
                                                                                                                      KERATINOCYTE; REPEAT.
                                                                                                                                                                                                                                                      PHILLIPS M., RICE R.H.,
                                                                                                                                                                                                                                                                                 TISSUE=VAGINAL FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                               INVOLUCRIN
                                                                                                                                                                                                                                                                                                                                                                                                                              INVO_SAGOE
                                                                                                                                PROSITE; PS00795; INVOLUCRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 lvrlrdlsahdkhdiqklskelemkrsevtelertkeklsa-kideleaivadlqeqvda 484
  164
              229 eggselpeggrggpkylegeegglkhleegkgglkhleheegglelpegvggpkhlegle 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 LQQTLAQKDQVL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 ldlangakkevl 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 QHLVKEKLLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 a-lgaeemveqlaekkmeledkvklleeei-a-qlealeevheqlvesnheleldlre-e 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 LAVIKEWKSSPGSNIGSAPMALERNISEL-QIQAAVEATGDLEVDCYRAPCCESQEELAL 171
                                                                 Local Similarity
                                                                                                                                                           OTHER STRATIFIED SQUAMOUS
                                                                                                                                                                                                                                       BIOL. EVOL. 8:579-591(1991).
 ESQEELALQHLVKEKLLAQLEEKLRVFANIVAVLNK-EVEASHLALAASIHQS-QLDR-E 220
                                                                                                                                                M67477; M67477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN; MICROTUBULES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                     29;
                                                                                                       493 AA;
                                                                                                                                                                                                                                                                                                                                                                                        (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
56
134
255
994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
98
167
564
1124
                                                                                                                                                                                                                                                                                                                                                                          21, CREATED)
21, LAST SEQUENCE UPDATE)
24, LAST ANNOTATION UPDAT
                                                                 29.6%;
                                                                                                       57920 MW;
                                                                                                                                                                                                                                                                                                                                    CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147858
                                                                             3.8%;
                                                                                                                                                                                                                                                    DJIAN P., GREEN H.;
                                                  Score 112; DB 4; Le
Pred. No. 6.32e-02;
24; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115; DB 3; Pred. No. 2.65e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAP-GLY.
SER-RICH.
COILED COIL.
COILED COIL.
MW; 8197543 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYNEIN; COILED COIL; CYTOSKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER-RICH.
                                                                                                                                                            EPITHELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                   VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                       1086880 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>::</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               493 AA.
                                                                                                                                                                                                                                                                                                                                                                          UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                            Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.
                                                   6
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
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289 kqlehpeqqegqlkhleeeegqvkhlgeqeeqlkhleq 326

-HLLSLEQRVVELQQTLAQKDQV--LGKLEHSLRLMEE 255

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221

1006:47

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227

245

prvyntqlvklqtdh-lktlndfqkllgdinwirpyl 280

QRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFL 263

Matches

187

168

Best Local Query Match 01-JUL-1993 01-OCT-1994 P31623; 01-JUL-1993 POL JSRV HYDROLASE; HSSP; P03366; 3HVT. J. VIROL. EMBL; M80216; M80216. YORK D.F., VIGNE R., VIRIDAE; SS-RNA SHEEP PULMONARY ADENOMATOSIS VIRUS POL POLYPROTEIN -!- THIS PROTEIN IS PROBABLY EXPRESSED AS A FUSED ÆDLINE; SEQUENCE FROM N.A. ENTIVIRINAE. !- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING. qlylvhymddillahtdehl-lyqaf-silkqhlslnglviadekiqthfpynylgfsly 244 C42740; GNMVJA. ELALQHLVKEKLLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHL-LSLE 226 S39397; S39397. 24; Similarity 24.7%; 92333675. -:: = 66:4930-4939(1992). RNA-DIRECTED DNA POLYMERASE; 870 AA; 99312 MW; 3962218 ((REL. 26, CREATED)
(REL. 26, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE) Conservative STANDARD; ENVELOPED (REVERSE TRANSCRIPTASE <u>..</u> VERWOERD D.W., QUERAT G.; VIRUSES; POSITIVE-STRAND; RETROVIRIDAE; Score 112; DB 6; Pred. No. 6.32e-02; PRT; Mismatches (JAAGSIEKTE SHEEP 870 ; NUCLEASE; (EC 2.7.7.49); ENDONUCLEASE). ⋧ 42; Length 870; Indels POLYPROTEIN GAG-PRO-PRO RETROVIRUS) 4; Gaps 4

RESULT
ID PO
AC CO
OC SI
OF OC
OC CC

(JSRV)

Ş 밁 Ş 뭐 Query Match Best Local S Matches 01-MAR-1992 01-MAR-1992 01-DEC-1992 VARSPLIC CONFLICT SEQUENCE INVO AO: P24708; TSENG H., GREEN H.;

MOL. BIOL. EVOL. 6:460-468(1989).

-!- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO DOMAIN DOMAIN CELL EUTHERIA; PRIMATES EUKARYOTA; METAZOA; AOTUS TRIVIRGATUS (NIGHT MONKEY) (DOUROUCOULI) DOMAIN DOMAIN PIR; S22695; S22695. MIM; 179838; 11TH EDITION. PROSITE; PS00845; CAP_GLY. EMBL; X64838; X64838. EMBL; M97501; M97501. -!- ALTERNATIVE PRODUCTS: IT IS PROBABLE THAT THE TWO FORMS OF THE PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING OF A SINGLE GENE. CYTOSKELETON.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES. PIERRE P., SCHEEL J., MEDLINE; SEQUENCE FROM N.A. INVOLUCRIN DOMAIN CYTOSKELETON; MICROTUBULES; DOMAIN ALTERNATIVE SPLICING. -!- SIMILARITY: CONTAINS A LARGE COILED-COIL ALPHA HELICAL DOMAIN -!- SIMILARITY: CONTAINS A CAP-GLY DOMAIN. -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE SEQUENCE FROM N.A. EMBO J. 11:2103-2113(1992) 222 509 alrvqe-vaelrrrl-esnkpagdvdmslsllqeis 542 165 451 tkgdletqtklehari-keleqsl-lfektkadklqreledtrvatvseksrimelekdl 508 10 STRUVTURALLY SIMILAR TO THOSE FOUND IN IF AND MYOSINS OF HODGKIN'S DISEASE. AOTTR LLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEAS SQEELALQ-HLVKEKLLAQLEEKLRVFANIVAV-LNKEVEASHLA-LAASIHQSQLDREH 221 70:887-900 (1992) Similarity 25.0%; 24; 92405160. 90014142. 1408 457 (REL. (REL. 78 143 232 304 852 = Conservative STANDARD; AA; 160989 21, 21, 24, 120 204 274 274 331 1145 1421 491 - CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 3.8%; LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) CREATED) RICKARD J.E., Score 113; DB 7; 1 Pred. No. 4.74e-02; 31; Mismatches 34: ₹ • HEPTAD REPEAT PATTERN; MISSING (IN SHOR D -> E (IN REF. MW; 9446135 CN; ссис-вох. COILED COIL IF-LIKE REGION SER-RICH. CAP-GLY. <u>--</u> SER-RICH. PRT; KREIS T.E.; 544 (IN SHORT FORM) ¥. 257 = :: 34; <u>2</u> Length 1427; Indels :: 7. PROTEIN Gaps --

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Qy Db	M 8 Q	SQ	ΨT	ŦŦ	FT	FT	FT	FΤ	FT	FΤ	FT	Ŧ	FT	FT	FT	Ŧ	
444 gqt : 279 GRT	Query Match Best Local Matches	SEQUENCE	CARBOHYD	CARBOHYD	CARBOHYL	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	METAL	METAL	ACT_SITE	METAL	DOMAIN	DOMAIN	
-tvysppfys ::: : : vslfspafyj	3.6%; Query Match Best Local Similarity 34.8%; Matches 24; Conservative	668 AA;	592	547	528	437	422	316	219	Ī	163	157		153	261	65	
sk-gyaf- : : AKYGYKLC	3.6%; 34.8%; rvative		592	547	528	437	422	316	219	193	163	157	154	153	430	260	
444 gqt-tvysppfyssk-gyafqinldltsp-tnvglyfhlisganddqlqmpcpmqq 496 : ::: : : : :: :: ::: : :: : 279 GRTVSLFSPAFYTAKYGYKLCLRLYINGDGSGKKTHLSLFIVIMRGEYDALLPMPF-RNK 337	; Score 106; DB 5; Length 668; ; Pred. No. 3.44e-01; 20; Mismatches 17; Indels 8; Gaps 6;	75050 MW; 2365479 CN;	POTENTIAL.	ZINC (CATALYTIC) (BY SIMILARITY).	ZINC (CATALYTIC) (BY SIMILARITY).	BY SIMILARITY.	ZINC (CATALYTIC) (BY SIMILARITY).	MAM.	CATALYTIC (ASTACIN DOMAIN).								

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338 VTFMLLDQN 346
                       497
                      atmtlldqn 505
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RESULT
                                                                                                                                                                                                                                                                                 01-AUG-1991 (REL. 19, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                          STRAIN=K12;
                                                                                                                                                                                                                                                              AEROBIC RESPIRATION CONTROL SENSOR PROTEIN ARCB
                                                                                                                                                                                                                                                                                                                                                  P22763;
                                                                                                                                                                                                                                                                                                                                                                        ARCB
                                        MOL. MICROBIOL. 4:715-727(1990).
                                                         MEDLINE; 90355832.
                                                                                                                                                                           ENTEROBACTERIACEAE
                                                                                                                                                                                             PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                  ESCHERICHIA COLI.
                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        ECOLI
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                           FUJIWARA T., LIN E.C.C.;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                          776 AA.
                                                                                                                                                                                                                                                            (EC 2.7.3.-).
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PLUNKETT G. III;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: MEMBER OF THE TWO-COMPONENT RECULATORY SYSTEM ARCB/ARCA. STRAIN=K12 / MG1655; MODULON. ACTIVATES ARCA BY PHOSPHORYLATION.

EMBL; X53315; X53315. (PROBABLE).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE -!- SIMILARITY: IN ITS C-TERMINUS, TO THE N-TERMINAL REGION -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE KINASES REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS

ECOGENE; EG10062; ARCB PIR; S11794; RGECAR. EMBL; U18997; U18997.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993
01-JUL-1993
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                       CENE_HUMAN
Q02224;
                                                                                                                                                                                                        - i - 1
NP_BIND
             DOMAIN
                         DOMAIN
                                                                                 EMBL; 215005; 215005.
PIR; S28261; S28261.
MIM; 117143; 11TH EDITION.
                                                                                                                                                                                                                           THROWER D.A., JORDAN M.A., SCHAAR B.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                           ÷
                                                                                                                                                                                                                                                                              YEN T.J., LI G., SCHAAR B NATURE 359:536-539(1992).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                        CENTROMERIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                CELL CYCLE;
                                                           MOTOR PROTEIN; CELL DIVISION;
                                                                                                                      -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                        MEDLINE; 95196755.
                                                                                                                                                                                                                                                       CHARACTERIZATION
                                                                                                                                                                                                                                                                                                     MEDLINE; 93024922.
                                                                                                                                                                                                                                                                                                                                         EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                      DOMAIN
                                                                        PROSITE; PS00411; KINESIN MOTOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SENSORY TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 Q-KDQVLGKLEHSLRIMEEASFDGTFL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 qlkieikereetqiqleqqssflrsfl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 vveqleesrqrlsrlvqkle-emrerdlslnvqlkdniaqlnqeiavrekaeaelqetfg 134
                                                                                                                                                                            FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
                                                                                                                                           SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE,
                                                                                                                                 QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
                                                                                                                                                                     AND/OR SPINDLE ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRV-VELQQTLA 237
                                                                                                                                                                                                                    14:918-926(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 24.1%;
 336
2472
86
; CENTROMERE.

1 335

336 2471

2472 2663

86 93
                                                                                                                                                                                                                                                                                                                                                                                                (REL. 26, (REL. 26, (REL. 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
51
58
78
78
269
269
292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                       SCHAAR B.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
50
57
77
776
515
515
292
                                                                                                                                                                                                                                                                                                                                                                                       m
                                                                                                                                                                                                                                                                                                                                                  CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
                                                                                                                                                                                                                                                                                                                                                                                      (CENP-E PROTEIN).
                                                                                                                      TO THE KINESIN-LIKE PROTEINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 105; DB 1;
Pred. No. 4.53e-01;
32; Mismatches 31
MECHANOCHEMICAL (MOTOR).
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMITTER DOMAIN (POTENTIAL).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

G -> GTG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                           ATP-BINDING;
                                                                                                                                                                                                                                                                                         SZILAK I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> GTG (IN REF. 1).
3085590 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTION REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2663 AA
                                                                                                                                                                                                                             YEN T.J., WILSON L.;
                                                                                                                                                                                                                                                                                         CLEVELAND D.W.;
                                                           COLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 776,
                                                          COIL;
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Best Local Similarity
                                                                             PC17_HUMAN
Q01850;
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01-DEC-1992
                       01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
PARAMEOPLASTIC CEREBELLAR DEGENERATION-ASSOCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1773 qeelriahmhlkeqqetidklrgivsektdklsnmqkdlensnaklqekiqelkanehql 1832
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EUTHERIA; PRIMATES.
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            PCD17.
                                                                                                                                                                                                                                                                                                                                                             EMBL; M67478; M67478
                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO
MEMBRANE PROTEINS BY TRANSCLUTAMINASE. ALL THAT RESULTS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHILLIPS M., RICE R.H., DJIAN P., GREEN H.; MOL. BIOL. EVOL. 8:579-591(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92114750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=ESOPHAGEAL FIBROBLAST;
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                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00795; INVOLUCRIN.
                                                                                                                                                  219 R-E-HLLSLEQRVVELQQTLAQKDQVLGKLEH
                                                                                                                                                                           267 qqegqlehleqqegelkh-leqcegqlehleq
                                                                                                                                                                                                                                 207 eggegglelpegydgpkhleglekglehpeggegklkkleeeeeglkhleggeeglkhle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 QEELALQHL-VKEKL--LAQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 LSLEQRVVELQQTLAQKDQVLGKL-EHSLRL 252
                                                                                                                                                                                                                                                                                                                                                                        FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE. TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIA.
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21, LAST SEQUENCE UPDATE)
24, LAST ANNOTATION UPDAT
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                         DEGENERATION-ASSOCIATED ANTIGEN.
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Pred. No. 2.61e-01
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HOMO SAPIENS (HUMAN).

5

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91083322.
RA SAKAI K., MITCHELL D.J., TSUKAMOTO T., STEINMAN L.;
RA SAKAI K., MITCHELL D.J., TSUKAMOTO T., STEINMAN L.;
RR MEDLINE; 9108332.
RN MEDLINE; 101281; D12981.
DR PIR; A49833.
RN ANTIGEN; CEREBELLUM.
SQ SEQUENCE 443 AA; 50549 MW; 1032055 CN;
Ouery Match
Best Local Similarity 26.1%; Pred. No. 7.82e-01;
Matches 30; Conservative 30; Mismatches 44; Indels 11; Gaps 10;
Matches 30; Conservative 30; Mismatches 44; Indels 11; Gaps 10;
Matches 30; Conservative 30; Mismatches 44; Indels 11; Gaps 10;

Db 13 lqqdlqlaaelgktlldrntele-dsvqqmyttnqeqlqeieyltkqvellrqmneqhak 71
i:::| :| : :| | : :| | : :| | | : :|

Search completed: Tue Dec 10 07:03:42 1996 Job time : 16 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:03:59 1996; MasPar time 17.22 Seconds 603.847 Million cell updates/sec

Tabular output not generated.

>US-08-446-915-2 (1-409) from US08446915.pep 2945

Description: Perfect Score:

1 MASSSAPDENEFQFGCPPAP.....KHAYVKDDTMFLKCIVDTSA 409

Scoring table: PAM 150 Gap 11

Searched: 82130 seqs, 25426960 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir47

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc 14:unrev

Statistics: Mean 47.486; Variance 124.260; scale 0.382

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.
1 2 2 3 4 4 4 5 5 7 7 7 10 11 11	!
2589 956 794 148 148 127 120 113 115 115 115	Score
87.9 32.5 5.0 4.9 4.3 3.9 3.9 3.9	Query Match
9 416 5 501 7 568 0 760 9 748 3 1048 3 1048 1 2291 1 2291 1 2319 9 1319 9 3259 9 3259	% Query Match Length DB
6 11 1 12 0 12 0 12 8 13 1 15 1 1 5 1 1 5 1 1 1 1 1 1 1 1 1 1 1	h DB
B55649 S56163 A55649 A40196 S24134 BVECSC A46147 S39464 A28313 S37536 S49383	ID
TNFR-associated prot tumor necrosis facto TNFR-associated prot meprin A (EC 3.4.24. endopeptidase 2 (EC sbcC protein - Esche spectrin beta chain PABA peptide hydrola glued protein - frui macrogolgin - human giantin - human meprin A (EC 3.4.24.	Description
0.00e+00 3.02e-125 9.73e-100 6.60e-05 1.93e-04 1.57e-02 8.87e-02 1.15e-01 2.96e-01 2.96e-01 7.59e-01	Pred. No.

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0 A45592 0 A43360		-		1 A41642	7 526365		8 F64058	3 RQECN	8 S03744	7 S03214	2 A36014	5 A47297	3 TNBEEH					1 A40448	1 UFEC	1 A49833	5 C24263	5 A24263	2 S28261	1 A43336	3 RGECAR		4 A42908		_	1 S22695	3 GNMVJA
liver stage antigen inositol 1,4,5-trisp	dynein-associated pr	myosin beta heavy ch	TATA element modulat	dynactin - chicken	P100 protein - Therm	ethylene-response pr	ä	_	•		myosin heavy chain,	myosin heavy chain f	Ĩ.	bsg25D protein - fru	CHO2 antigen - Chine	kinesin-like motor p	intermediate filamen	DNA-binding protein	fumarate hydratase (autoantigen recogniz	myosin heavy chain,	myosin heavy chain,	kinesin-related prot	microtubule-vesicle	aerobic respiration	ta	meprin A (EC 3.4.24.	P63 protein - human	hypothetical protein	in - human	pol polyprotein - sh
7.31e+00 1.13e+01	7.31e+00	9.09e+00	9.09e+00	1.13e+01	7.31e+00	7.31e+00	9.09e+00	7.31e+00	9.09e+00	9.09e+00	4.70e+00	5.86e+00	4.70e+00	3.76e+00	3.76e+00	3.76e+00	3.76e+00	4.70e+00	4.70e+00	4.70e+00	3.76e+00	4.70e+00	1.91e+00	3.00e+00	3.00e+00	1.91e+00	2.40e+00	2.40e+00	9.58e-01	4.75e-01	6.01e-01

ALI GNMENTS

2 ASSSAPDENEFQFGCPPAPCQDPSEPRVLCCTACLSENLRDDEDRICPKCRADNLHPVSP

61

Dec 10 06:47

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KEYWORDS
SUMMARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATE_NAMES
                   Query Match 32.5%;
Best Local Similarity 53.6%;
                                                                                                                                                                                                                                                                   #accession
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                                                                                                                                                                                                                                                                                                                            submission
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                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                      ##cross-references EMBL:U12597
                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
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 120;
                                                                                                                                                                                                                                                                                Song, H.Y.; Donner, D. submitted to the EMBL Data Library, July 1994 Association of a RING finger protein with the domain of the human type 2 TNF receptor.
                                                                                                                                                                                     S58926
                                                                                                                                                                                                                                                                   S58925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S56163
                                                                              zinc finger #length 501 #molecular-weight 55842 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song, H.Y.; Donner, D.B.
Biochem. J. (1995) 309:825-829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNF receptor-associated protein
                                                                                                                                                                                                                                                                                                                                                                      S58925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Association of a RING finger protein with the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S56163; S58925; S58926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-Oct-1995 #sequence_revision 01-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S56163 #type complete tumor necrosis factor receptor-associated protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S56163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Homo sapiens #common_name man
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain of the human type-2 tumour necrosis factor receptor.
                                                                                                                                         1-342, 'RPFQAQCGHRYCSFCLASIL', 363-501 ##label
                                                                                                                                                                                                                         1-42, 63-342, 363-501 ##label SOF
                                                                                                                                                                                                                                                                                                                                                                                                            1-501 ##label SON
                   Score 956; DB 12;
Pred. No. 3.02e-125;
 Mismatches 45;
                                        Length 501;
 Indels
                                                                                                                                                                                                                                                                                                     cytoplasmic
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 Gaps
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Ş 밁 183 LEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQV 242 275 lekktatfenivcvlnrevervamtaeacsrqhrldqdkiealsskvqqlersiqlkdla US-08-446-915-2 rpr

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Q 243 LGKLEHSLRIMEEASFDGTFIWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRL 302

Ş 밁

맑 455 sfqrpvndmniasgcplfcpvskmea-knsyvrddaifikaivd 497
|||||| : |:|||||| |:||::||:||:||:|| |||
363 SFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406

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ALTERNATE NAMES w CD40-binding protein TNFR-associated protein LAP1 -#type complete human

Ş 밁 Ó 밁

> 308 241

rlylngdgtgkrthlslfivimrgeydallpwpfrnkvtfmlldqnnrehaidafrpdls 367

RLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPDLS 360

QVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCL

300 307 240 247 180

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361 368 301

SASFORPOSETNVASGCPLFFPLSKLOSPKHAYVKDDTMFLKCIVDTSA 409 밁

188

aelegklrvfenivavinkeveashlalatsihqsqldrerilsleqrvvelqqtlaqkd

AQLEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKD

Ś 밁 Ś 밁 Ş

121

128

arlgcglesgpmaleqnlsdlqlqaavevagdlevdcyrapcsesgeelalqhfmkekll 187

GSPL-TQEKVHSDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKEWK 120 gsrirtqekahpevaeagigcpfagvgcsfkgspqsvqehevtsqtshlnlllgfmkqwk 127

SSPGSNLGSAPMALERNLSELQLQAAVEATGDLEVDCYRAPCCESQEELALQHLVKEKLL

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248 181

ORGANISM ACCESSIONS #formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995
05-Apr-1995 A55649; A55135 #text_change

REFERENCE #journal
#title #authors Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E. Cell (1995) 80:389-399 A55649

The Epstein-Barr virus transforming protein LMP1 engages

signaling proteins for the tumor necrosis factor receptor

#accession ##molecule_type mRNA A55649 family.

##cross-references GB:U19260 ##residues 1-568 ##label SOM

##note A55135 nucleotide sequence not given

REFERENCE ftitle. **f** journal lauthors Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M. J. Biol. Chem. (1994) 269:30069-30072

A novel RING finger protein interacts with the cytoplasmic

faccession A55135 domain of CD40.

##cross-references GB:U15637 ##residues ##molecule_type mRNA 1-133,135-404,'G',406-568 ##label HUA

given

KEYWORDS ##note coiled coil nucleotide sequence not

FEATURE 53-91 #region RING-finger motif
#length 568 #molecular-weight 64490

SUMMARY #checksum

뮹 Matches Query Match 27.0%; Best Local Similarity 38.8%; 189 lqkhedtdcp-cvvvscphkcsvqtllrselsahlsecvnapstcsfkrygcvfqgtnqq 247 149; Conservative Score 794; DB 11; Pred. No. 9.73e-100; 93; Mismatches 118; Length 568; Indels 24; 18;

밁 Ş 248 ikaheassavqhvnll----kewsnslekkvsllqnesveknksiqslhnqi-csfeiei 302 40

97 MQEHEATSQSSHLYLLIAVIKEWKSSPGSNLGSAPM-ALERNLSELQLQAAVEATGDLEV

155

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US-08-446-915-2 rpr

CLASSIFICATION FEATURE 1-33 RESULT ENTRY Ş 맑 S 밁 Ş 뭐 Ş 맑 Ş 밁 DATE SUMMARY REFERENCE REFERENCE ACCESSIONS ORGANISM ALTERNATE_NAMES 87-273 34-77 78-760 # journal # journal #authors #accession cross-references MUID: 92042028 #authors cross-references MUID:92250517 ##cross-references GB:M74897; GB:M74238 482 385 KLQSPKHAYVKDDTMFLKCIVDTS 408 542 vleng--tyikddtifikvivdts 563 208 363 elesvdksagqvarntgl-lesqlsrhdqmlsvhdirladmdlrfqvletasyngvliwk 421 156 DCYRAPCCESQEE-LALQHLVK-E-KLLAQLEEKLRVF-AN-IVA-VLNKEVEA--SHLA 207 ##residues **molecule_type mRNA ##note ##cross-references GB:M74897 ##molecule_type mRNA 303 erqkemlrnneskilhlqrvidsqaeklkeldkeirpfrqnweeadsmkssveslqnrvt 362 ##residues YDALLPWPFRNKVTFMLLDQ-NNREHAIDAFRPDLSSASFQRPQSETNVASGCPLFFPLS 384 LAASIHQS--QLDREHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFLWK 265 #superfamily astacin homology; MAM homology J.S.; Flannery, A.V.; Beynon, R.J. J. Biol. Chem. (1991) 266:21381-21385 Dumermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond, J.S.; Flannery, A.V.; Beynon, R.J. A40195 B41196 The astacin family of metalloendopeptidases A41196 The alpha subunit of meprin A. Molecular cloning and sequencing, differential expression in inbred mouse J. Biol. Chem. (1992) 267:9185-9193 Jiang, W.; Gorbea, C.M.; Flannery, A.V.; Beynon, R.J.; Grant, A40195 A40195; B41196 #formal_name Mus musculus #common_name house mouse
16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change endopeptidase-2 A40195 #type complete meprin A (EC 3.4.24.18) alpha chain precursor -#length 760 strains, and evidence for divergent evolution of the alpha and beta subunits. G.A.; Bond, J. 23-Mar-1995 1-760 ##label JIA part of this sequence, including the amino end of the #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product meprin A alpha chain #status experimental 77-275 ##label DUM #domain MAM homology #label MAM #domain astacin homology #label AST\ #label MAT\ mature protein, was confirmed by protein sequencing #molecular-weight 85702 #checksum 4733

Dec 10 06:47 US-08-446-915-2 ppr

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Ş TITLE ENTRY RESULT Ş В Q 밁 CLASSIFICATION 밁 В REFERENCE ORGANISM SUMMARY FEATURE KEYWORDS REFERENCE ORGANISM ALTERNATE_NAMES ACCESSIONS ACCESSIONS Matches Query Match 4.9%; Best Local Similarity 26.9%; 76-262 265-434 156,160,166 Matches Query Match 5.0%; Best Local Similarity 32.9%; #journal
#title #authors *accession cross-references MUID:92371675 447 vwtirnisqilentv--kgdklvsprfynse-gygvgvtlypngritsnsgllgltfhly 503 493 sgdndvilewpveneqaimtildqepdarnrmslslmfttskyq 536 504 sgdndailewpvenrqaimtildqe 528 |: ||:| || |: ::| :|||: 323 RGEYDALLPWPFRNKVTFM-LLDQNNREHAIDAFRPDLSSASFQ 365 263 LWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRLYLNGDGSGKKTHLSLFIVIM 322 ##residues ##molecule_type mRNA 323 RGEYDALLPWPFRNKVTFM-LLDQN 263 LWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCLRLYLNGDGSGKKTHLSLFIVIM 32 ##status S 28; 28; S24134 S24134 S24134 endopeptidase 2 (EC 3.4.24.-) - rat
endopeptidase 24.18 #superfamily MAM homology; astacin homology #formal_name Escherichia coli 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change BVECSC #type complete sbcC protein - Escherichia coli #binding_site zinc (His) #status predicted #length 748 #molecular-weight 85138 #checksum hydrolase; metalloprotein; proteinase; zinc Corbeil, D.; Gaudoux, F.; Wainwright, S.; Ings A.J.; Boileau, G.; Crine, P. FEBS Lett. (1992) 309:203-208 Molecular cloning of the alpha-subunit of rat #formal_name Rattus norvegicus #common_name Norway rat
02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change JS0350; A43750; S27548; S06604 JS0349 Conservative Conservative 05-May-1994 hybridization endopeptidase-24.18 (endopeptidase-2) and co-localization with endopeptidase-24.11 in rat kidney by in situ 19-Oct-1995 1-748 ##label COR preliminary #domain MAM homology #label MAM\ #domain astacin homology #label AST\ :: :: #type complete Score 144; DB 12; Length 748; Pred. No. 1.93e-04; Score 148; DB 12; Pred. No. 6.60e-05; 29; Mismatches 43; Indels 22; Mismatches 31; Indels Length S.; Ingram, J.; Kenny, 4. 4. 2333 Gaps Gaps 4. Ψ

#authors

Naom, I.S.; Morton, S.J.; Leach, D.R.F.; Lloyd, R.G.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 sqqtsdrehlrqwqqqlthaeqklnalaaitltltad-evat-alaqhaeqrpl-rqhlv 429
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This protein interacts with long DNA palindromes and reduces the viability of the carrier DNA; it is also involved in genetic
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##residues 379-1048 ##label RE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily sbcC protein coiled coil; DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mapping, sequence, and apparent lack of function of aral, gene of the Escherichia coli arabinose regulon. A43750
               Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6187-6191
The complete sequence of Drosophila beta-spectrin reveals supra-motifs comprising eight 106-residue segments.
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                                                                                                                                                                                   #domain nucleotide-binding fstatus predicted flabel NBI
flength 1048 fmolecular-weight 118720 fchecksum 3454
                                                                                                     Byers, T.J.; Brandin, E.; Lue, R.A.; Winograd,
                                                                                                                             A46147
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FEATURE 49-267 RESULT ENTRY В TITLE S ₽ Ş Ş 밁 SUMMARY CLASSIFICATION #superfamily spectrin beta-G chain; alpha-actinin REFERENCE CLASSIFICATION REFERENCE ORGANISM ACCESSIONS Matches Query Match 4.1%; Best Local Similarity 27.7%; 417-522 #journal
#title #journal
#title 2146-2257 #accession #accession #authors #accession #authors ##molecule_type mRNA 251 RIMEEASFDGTFLWKITNVTK 271 850 klmsea--dgveqw-ikektk 867 192 NIVAVLNKEVEASHLALAASIHOSQLDREHLLSLEQRVVELQQ-TLAQKDQVLGKLEHSL 250 134 LERNISELQIQAAVEATGDLEVDCYRAPCCE--SQEELAIQHIVKEKILAQLEEKIRVFA 191 737 lenaveyfqlfadaddvdnwmldtlrivssedvgrdeanvqsllk-kh-kdvadelknya 794 ##residues ##molecule type mRNA ##status ##residues ##status 795 evidalhkqae-s-1klnea-ekanvdk-rleaidnrykeltelaklrkqrlldals1-y 849 ##cross-references GB:M92288 ##note ##cross-references NCBIP:108607 ##residues ##molecule_type DNA #status 39; A33657 #superfamily MAM homology; astacin homology S39464 Goldstein, L.S.B. J. Cell Biol. (1989) 109:1633-1641 A46147 Cloning of the PABA peptide hydrolase alpha subunit (PPH-alpha) from human small intestine and its expression in COS-1 cells. S39464 Byers, T.J.; Husain-Chishti, A.; Dubreuil, R.R.; Branton, D.; FEBS Lett. (1993) 335:367-375 PABA peptide hydrolase alpha chain — human #formal_name Homo sapiens #common_name man 19-May-1994 #sequence_revision 17-Nov-1995 #domain pleckstrin repeat homology #label PLK
#length 2291 #molecular-weight 265785 #checksum 9818 A33657 Dumermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang, W.; S39464 539464 Conservative Sterchi, E.E. 01-Dec-1995 spectrin/dystrophin repeat homology actin-binding domain homology; pleckstrin repeat homology; 1-714 ##label DUM 1-800 ##label BY2 preliminary preliminary #domain spectrin/dystrophin repeat homology #label SN2\ #domain alpha-actinin actin-binding domain homology sequence extracted from NCBI backbone 1-2291 ##label BYE preliminary #label ACT\ #type complete Score 120; DB 5; Length 2291; Pred. No. 8.87e-02; ----------36; Mismatches 53; Indels 13; Gaps #text_change 11;

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Db 541 Idlangakkev1 552 : :: : Qy 232 LQQTLAQKDQVL 243
Db 485 a-lgaeemveqlaekkmeledkvklleeei-a-qlealeevheqlvesnheleldlre-e 540
Db 426 lvrirdlsahdkhdiqklskelemkrsevtelertkeklsa-kideleaivadlgegvda 484
Query Match 3.9%; Score 115; DB 10; Length 1319; Best Local Similarity 25.0%; Pred. No. 2.96e-01; Matches 33; Conservative 35; Mismatches 58; Indels 6; Gaps 6;
397,590,771,888, 980,1110,1127,1133, \$binding_site carbohydrate (Asn) (covalent) \$status 1142 predicted \$SUMMARY \$length 1319 \$molecular-weight 147858 \$checksum 8175
GENETICS #introns 18/2; 479/3 KEYWORDS glycoprotein FRATURE
#accession AR8313 ##molecule type DNA; mRNA ##residues 1-1319 ##label SWA the authors' translation is inconsistent with the ##note nucleotide sequence in the region 907-925
<pre>#authors Swaroop, A.; Swaroop, M.; Garen, A. #journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6501-6505 #title Sequence analysis of the complete cDNA and encoded</pre>
RESULT 9 ENTRY A28313 #type complete TITLE glued protein - fruit fly (Drosophila melanogaster) ORGANISM #formal name Drosophila melanogaster DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Dec-1993
Db 458 sgendailewpvenrqviitildqe 482 : : : : : :
Db 403 vwtvrnfs-qvlent-skgdklqsprfynse-gygfgvtlypnsressgylrla-fhvc- 457 : : : : : : : :
Query Match 4.0%; Score 119; DB 11; Length 714; Best Local Similarity 34.1%; Pred. No. 1.13e-01; Matches 29; Conservative 19; Mismatches 31; Indels 6; Gaps 6;
FEATURE 43-229 #domain astacin homology #label AST\ 232-401 #domain MAM homology #label MAM SUMMARY #length 714 #molecular-weight 80703 #checksum 3852

RESULT 10

Matches 26; Db 208 qtqaeq :: Qy 164 ESQEEL Db 267 slugra Qy 222 LLSLEQ	sion tatu oleo esion rosu rosu atch	ORGANISM DATE ACCESSIONS REFERENCE # authors # journal # title	7 2 2	Query Match Best Local Sim Matches 26; Db 208 qtqaeq :: Qy 164 ESQEEL	#accession S37536 ##status ##molecule_type_mR ##residues 1- ##cross-references SUMMARY #length	ACCESSIONS REFERENCE #authors #submission	ENTRY TITLE ORGANISM DATE
ekd-arfeto	nne protein (glantin). Liminary R 1259 #label SEE CB:X75304 CB:X75304 3259 #molecular-weight 376075 #checksum 4495 3.9%; Score 115; DB 11; Length 3259; 27.7%; Pred. No. 2.96e-01;	name Homo (1995 #seque) 1995 #seque) 1995 #seque) 1995 H.P.; Schriths, G.; Re 1ths, G.; Re 1ths, G.; Re 1ths, G.; Re	<pre>slvgraqvvdllqqeltaaeqrnqilsqqlqqme 300 : : : : : LLSLEQRVVEL-QQTIAQKDQVLGKLEHSIRIME 254 1</pre>	tch 3.9%; Score 115; DB 11; Length 3259; al Similarity 27.7%; Pred. No. 2.96e-01; 26; Conservative 24; Mismatches 40; Indels 4; Gaps 4; gtqaeqaaqqyvrekd-arfetqyrlhedellqlvtqadvetemqqklrvlqrkleehee 266 ::	in. in. in. eliminary eliminary NA 3259 ##label EMBL:X75304 3259 #molec	95 ; Schranz, P.; Schroeter, H.; Wiem , G.; Renz, M. o the EMBL Data Library, September	\$37536 #type complete macrogolgin - human #formal name Homo sapiens #common name man 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

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Best Local Similarity 35.4%;
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                                                                                                                                                         ##molecule_type genomic RNA
##residues 1-870 ##label YOR
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                                                                                   ##cross-references GB:M80216
T This protein is likely to be expressed as a gag-pol polyprotein.
The precise boundary between RNA-directed DNA polymerase and
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                                                                   endonuclease has not been determined.
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                                                                                                                                                                                                      C42740
                                                                                                                                                                                                                                                               Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and endogenous type D and B retrovirus of sheep
                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name sheep pulmonary adenomatosis virus
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
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16-Feb-1995 #sequence_revision 12-May-1995 #text_change
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J. Virol. (1992) 66:4930—4939
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Pred. No. 7.59e-01;
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                                                                                                                                                                                                                                                                                                                                                            222 LLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEAS 257
                                                                                                                                                                                                                                                                                                                  509 alrvqe-vaelrrrl-esnkpagdvdmslsllqeis 542
                                                                                                                                                                                                                                                                                                                                                                                                           451 tkgdletqtklehari-keleqsl-lfektkadklqreledtrvatvseksrimelekdl 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBi:x64838
Y #length 1427 #molecular-weight 160989 #checksum 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 QRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 prvyntqlvklqtdh-lktlndfqkllgdinwirpyl 280
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Similarity 24.7%;
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                                                                   17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bilbe, G.; Delabie, J.; Brueggen, J.; Richener, H.;
Asselbergs, F.A.M.; Cerletti, N.; Sorg, C.; Odink, K.;
Tarcsay, L.; Wiesendanger, W.; DeWolf-Peeters, C.; Shipman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Restin: a novel intermediate filament-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Homo sapiens #common_name man
04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
18-Jun-1993
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                                                                                                                                                           hypothetical protein 1 - African malaria mosquito (fragment)
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Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins,
                                                                                                                                !formal_name Anopheles gambiae #common_name African malaria
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                                                                                                               mosquito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches 34;
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SUMMARY Query Match 3.7%; Score 110; DB 10; Length 613; Best Local Similarity 32.0%; Pred. No. 9.58e-01; Matches 24; Conservative 17; Mismatches 31; Indels 3; Gaps 195 aaapmmtaggahssr 209 | : : || | 237 AQKDQVLGKLEHSLR 251 ##molecule_type DNA
#fresidues 1-613 #flabel BES
#fcross-references EMBL:M93690
RY #length 613 #checksum 108 μ

Search completed: Tue Dec 10 07:04:22 1996 Job time : 23 secs.

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Dec 10 06:51

US-08-446-915-4 rpr

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intellicenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:07:14 1996; MasPar time 20.07 Seconds 634.805 Million cell updates/sec

Tabular output not generated.

>US-08-446-915-4 (1-501) from US08446915.pep 3702

Description: Perfect Score:

Sequence: 1 MAAASVTSPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 501

Scoring table: PAM 150 Gap 11

Searched: 82130 seqs, 25426960 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir47

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc 14:unrev

Statistics: Mean 48.057; Variance 117.898; scale 0.408

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ength DB	⊞	ID	Description	Pred. No.
_	3270	88.3	501 1	2	s56163	tumor necrosis facto	0.00e+00
2	986	26.6	416 1	-	B55649	TNFR-associated prot	1.74e-138
ω	806	21.8	568 1	_	A55649	TNFR-associated prot	3.03e-108
4	229	6.2	458	9	A29361	DG17 protein - slime	3.43e-16
Ç	162	4.4	700 1	_	S49383	meprin A (EC 3.4.24.	4.44e-07
6	162	4.4	760 12	~	A40195	meprin A (EC 3.4.24.	
ب	158	4.3		w	DDBY18	DNA repair protein R	
&	158	4.3	704 12	2	A48040	meprin beta chain pr	
9	157	4.2		4	A42908	meprin A (EC 3.4.24.	1.93e-06
10	155	4.2	748 1	2	S24134	endopeptidase 2 (EC	3.45e-06
11	153	4.1	1483	ω	RGBYH1	regulatory protein H	6.15e-06
12	153	4.1	1502 1	4	S59400	CYC1/CYP3 transcript	6.15e-06

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
104	104	105	104	104	107	107	106	107	109	107	111	110	111	112	112	110	110	114	113	114	114	120	119	119	120	127	127	127	126	135	139	141
2.8	2.8			2.8	2.9	2.9	2.9	2.9	2.9	2.9	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.1	3.1	3.1	3.1	3.2	3.2	3.2	3.2	3.4	3.4	3.4	3.4	3.6	3.8 8	3.8
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S33124	S28418	B43549	A43549	TMCHS1	S22028	S20486	S09228	S59296	JN0533	D39371	A47297	A33754	в33754	S44379	S42511	S51037	S06565	S34825	S28022	C24263	S23470	A54652	S51157	S05585	S28290	S55494	S57328	S57398	S06573	A44272	S39464	A47380
tpr protein - human	probable zinc-bindin	vimentin 4 - African	vimentin 1 - African	_	co .	paramyosin - fruit f	intermediate filamen	probable Zn-finger (finger protein pMLZ-	Ig V-region-like B-G	myosin heavy chain f	recombination-activa	bination-ac	RAG-1 protein - rabb	RAG-1 protein - rabb	zinc-finger protein		uvs2 protein - Neuro	outer membrane prote	myosin heavy chain,	beta-tropomyosin - A	breast/ovarian cance		tropomyosin - human	hypothetical protein	type zinc	1	NUVA protein - Emeri	finger protein (clon	photomorphogenesis r	PABA peptide hydrola	RING finger-containi
2.72e+00	2.72e+00	2.15e+00	2.72e+00	2.72e+00	1.33e+00	1.33e+00	1.69e+00	1.33e+00	8.23e-01	1.33e+00	5.05e-01	6.45e-01	5.05e-01	3.94e-01	3.94e-01	6.45e-01	6.45e-01	2.40e-01	3.08e-01	2.40e-01	2.40e-01	5.24e-02	6.77e-02	6.77e-02	5.24e-02	8.40e-03	8.40e-03	8.40e-03	1.10e-02	9.74e-04	3.24e-04	1.86e-04

ALI GNMENTS

##molecule_type_mtNNA ##residues 1-42 ##cross-references E #accession \$58926	##cross-re REFERENCE # authors # submission # description # accession	# journal Biochem. # title Associati domain # accession 556163 ##molecule_type_mRNA ##residues 1-50	RESULT 1 EMTRY TITLE ALTERNATE NAMES ORGANISM DATE ACCESSIONS REFERENCE
##molecule_type_mtNA ##residues 1-42,63-342,363-501 ##label SOW ##cross-references EMBL:U12597 cession S58926	##oross-references EMBL:U12597 NCE 558925 thors Song, H.Y.; Donner, D. bmission submitted to the EMBL Data Library, July 1994 scription Association of a RING finger protein with the cytoplasmic domain of the human type 2 TNF receptor. cession 558925	Song, H.Y.; Donner, D.B. Riochem. J. (1995) 309:875-879 Association of a RING finger protein with the cytoplasmic domain of the human type-2 tumour necrosis factor receptor. 556163 type mRNA 1-501 ##label SON	556163 #type complete tumor necrosis factor receptor-associated protein - human TNF receptor-associated protein #formal name Homo sapiens #common name man 10-oct-1995 #sequence_revision 01-Dec-1995 #text_change 01-Dec-1995 556163; S58925; S58926 556163

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Best Local Similarity 86.6%;
                                                                                                                      #authors
                                                                                          #journal
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##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                             eacsrqhrldqdkiealsskvqqlersiglkdlamadleqkvlemeastydgvfiwkisd
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                                                                                                                                                                                                                                                                                                                  knsyvrddaifikaivdltgl 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQKVSELEVSTYDGVFIWKISD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434;
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                                                         The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor
                                                                                        T.; Ware, C.; Kieff, Cell (1995) 80:389-399
                                                                                                       Mosialos, G.; Birkenbach, M.; Yalamanchili, T.; Ware, C.; Kieff, E.
                                                                                                                                    A55649
                                                                                                                                                                          23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
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               preliminary
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Pred. No. 0.00e+00;
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                 Query Match 21.8%;
Best Local Similarity 52.7%;
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Best Local Similarity 55.4%;
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1-133,135-404,'G',406-568 ##label
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                                                                                                                                        ##note
                                                                                                                                                      ##cross-references GB:U15637
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   98;
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A novel RING finger protein interacts with the cytoplasmic
                                                                                                                                                                                                                                                                                             A55135
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                                                                                                                      coiled coil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale,
T.; Ware, C.; Kieff, E.
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A55649
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23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
                                                                    #length
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   Conservative
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                                                                                                                                                                                                                                                                                                             nucleotide sequence not given
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yth 568  #molecular-weight 64490
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                Score 806; DB 11;
Pred. No. 3.03e-108;
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Pred. No. 1.74e-138;
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   Mismatches
   36;
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SUMMARY

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REFERENCE

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TITLE Dec 10 06:51 meprin A (EC 3.4.24.18) - human US-08-446-915-4.pr

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RESULT ENTRY В Ş 맑 REFERENCE REFERENCE ACCESSIONS ORGANISM ALTERNATE NAMES SUMMARY FEATURE CLASSIFICATION REFERENCE DATE ACCESSIONS ORGANISM Query Match Matches Query Match 4.4%; Best Local Similarity 33.3%; 71-257 # journal #authors cross-references MUID: 92250517 # journal #authors 260-429 #accession *accession #submission #authors description 481 sganddq1qwpcpwqqatmt11dqnpdirqrmsnq-rs-ittdpf 523 415 KGPNDALLQWPFN-QKVTLMLLDHN-N-REHVIDAFRPDVTSSSF 456 431 iwhirnft---q-figspngtlysppfyssk-gy-a-fqiyln---lahvtnagiyfhli 480 ##cross-references GB:M74897 ##residues ##molecule_type mRNA 355 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414 ##molecule_type mRNA ##status ##cross-references EMBL:X81333 ##residues 6 J.S.; Flannery, A.V.; Beynon, R.J. J. Biol. Chem. (1991) 266:21381-21385 A40195 G.A.; Bond, J.S. J. Biol. Chem. (1992) 267:9185-9193 endopeptidase-2 #superfamily MAM homology; astacin homology S49383 Cloning and the PABA-peptide hydrolase beta subunit: Dumermuth, E.; Sterchi, E.E.; Jiang, W.; A41196 The alpha subunit of meprin A. Molecular cloning Jiang, W.; Gorbea, C.M.; Flannery, A.V.; Beynon, R.J.; Grant, #length 700 #molecular-weight 79458 #checksum Eldering, J.A.; Groenberg, J.; Sterchi, E.E. submitted to the EMBL Data Library, September 1994 549383 A40195 A40195; B41196 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 549383 #formal_name Homo sapiens #common_name man
16-Feb-1995 #sequence_revision 12-May-1995 #text_change formal name Mus musculus #common name house mouse Conservative sequencing, differential expression in inbred mouse strains, and evidence for divergent evolution of the alpha and beta subunits. coexpression is required for plasma membrane localization of the alpha subunit in COS-1 cells. 23-Mar-1995 26-May-1995 1-760 ##label JIA part of this sequence, including the amino end of the #domain MAM homology #label MAM #domain astacin homology #label AST\ 1-700 ##label preliminary mature protein, was confirmed by protein sequencing Score 162; DB 11; Pred. No. 4.44e-07; = = = = Mismatches Length 700; Indels Wolz, 15; 916 Gaps

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Best Local Similarity 32.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #title The Saccharomyces cerevisiae RAD18 gene encodes a protein that contains potential zinc finger domains for nucleic acid binding and a putative nucleotide binding sequence #cross-references MUID:88303333
                                                               #submission
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                 ##molecule_type DNA
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##residues 1-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   S05802
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                                                           submitted to the Protein Sequence Database, March 1992
                                                                                                                                                                                                                                                                                                                                       Benit, P.; Chanet, R.; Fabre, F.; Faye, G.; Fukuhara, H.;
                                                                                                                              S19477
                                                                                                                                                                                                                                                                                             Yeast (1992) 8:147-153
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31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
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                                             S19481
                                                                                                                                                                                                                                                                        Sequence of the sup61-RAD18 region on chromosome III of
                                                                                                                                                                                                                                                                                                                                                              S22260
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                                                                                Fukuhara, H.; Mathieu, A.; Sor,
                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.
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Pred. No. 4.44e-07;
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Best Local Similarity 36.7%;
Matches 18; Conservative
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Matchen 2.7%;
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482 sganddqlqwpcpwqqatmtlldqnpdirqrmfnq-rsittdpt 524
                                                                         432 iwhiqnft---
                                                                                                                                                                                                                                                                                              ##residues 1-704 ##label
##cross-references GB:L15193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
                                        355 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414
                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                           ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 RIEAKYLCSACKNIIRRPFQAQCGHRYCSFCLTSILSSGPQNCAACVYE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 qldtllrchickdflkvpvltpcghtfcslcirthlnnqp-ncplclfe 68
                                                                                                                    34;
                                                                                                                                                                                                                                                                        #superfamily MAM homology; astacin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A48040 #type complete
meprin beta chain precursor - mouse
fformal name Mus musculus fcommon name house mouse
02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        뀱
                                                                                                                                                                                            $length 704  #molecular-weight 79585  #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning, expression, and chromosomal localization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. (1993) 268:21035-21043
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorbea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.;
Gilbert, D.J.; Jenkins, N.A.; Bond, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS0082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chanet, R.; Magana-Schwencke, N.; Fabre, Gene (1988) 74:543-547
                                                                                                                                                                                                                                                                                                                                                                               A48040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP; DNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISTA: RAD18
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily DNA repair protein RAD18
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                                                                                                                                                                                                                                                                                                                                                                                                 mouse meprin beta subunit.
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                                                                                                                                                                                                                                                                                                                                                         preliminary
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                                                                                                                                                                                                                                      #domain astacin homology #label AST\
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#region zinc finger motif\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 158; DB 3;
Pred. No. 1.44e-06;
                                                                                                                                                   Score 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches 14; Indels
                                                                                                                    34; Mismatches 22;
                                                                                                                                      Pred. No. 1.44e-06;
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                                                                                                                                                           DB 12;
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                                                                                                                    Indels 14; Gaps
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ACCESSIONS REFERENCE RESULT ENTRY Ş Ş 8 밁 SUMMARY ORGANISM ALTERNATE_NAMES FEATURE KEYWORDS CLASSIFICATION REFERENCE ORGANISM ACCESSIONS ALTERNATE_NAMES Query Match 4.2%; Best Local Similarity 40.0%; Matches 72-258 261-430 #authors # journal #journal #title cross-references MUID:92371675 faccession accession cross-references MUID: 92317075 lauthors 432 iwhiqnft---q-llgqqt-tvysppfyssk-gy-a-fqinl--ditsp-tnvglyfhli 480 |:|| |||| | |: |||:| 415 KGPNDALLQWPFN-QKVTLMLLDHN 438 481 sganddqlqwpcpwqqatmtlldqn 505 ##molecule_type mRNA ##status ##cross-references NCBIP:107784 10 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414 34; S24134 S24134 endopeptidase-2 beta chain; meprin beta chain; meprin-a beta Corbeil, D.; Gaudoux, F.; Wainwright, S.; Ingram, A.J.; Boileau, G.; Crine, P. FEBS Lett. (1992) 309:203-208 #domain MAM homology #label MAM
#length 668 #molecular-weight 75049 #checksum *superfamily meprin A; astacin homology; MAM homology A42908 heterodimer; hydrolase Johnson, G.D.; Hersh, L.B. J. Biol. Chem. (1992) 267:13505-13512 A42908 #type complete meprin A (EC 3.4.24.18) beta chain - rat 524134 Molecular cloning of the alpha-subunit of rat endopeptidase 24.18 (endopeptidase 2) and co-localization #formal_name Rattus norvegicus #common_name Norway rat 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change Conservative Cloning a rat meprin cDNA reveals the enzyme is a A42908 A42908 #formal name Rattus norvegicus #common_name Norway rat 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change hybridization. heterodimer. with endopeptidase-24.11 in rat kidney by in situ 19-0ct-1995 23-Mar-1995 sequence extracted from NCBI backbone 1-668 ##label JOH preliminary #domain astacin homology #label AST\ 23; Score 157; DB 4; Length 668; Pred. No. 1.93e-06; Mismatches 16; Indels 12; J.; Kenny, Gaps 9

##status

preliminary

FEATURE

1-148 59-98

KEYWORDS

DNA binding; heme binding; zinc finger

#region zinc finger CCCC motif\

#domain DNA-binding #status predicted #label DNA\
#domain GAL4 zinc binuclear cluster homology #lab

cluster homology

#superfamily regulatory protein HAP1; GAL4 zinc binuclear

CLASSIFICATION GENETICS

#gene

LISTA:CYP1; HAP1

##note

##cross-references EMBL:X13793

the sequence is from mutant CYP1-18

1-62, 'R', 64-144, 'T', 146-322, 'K', 324-454, 'S', 456-507, 'V', 509-586, 'N', 588-882, 'D', 884-959, 'H', 961-1150, 'D', 1152-1156, 'S', 1158-1304, 'N', 1305-1483 #flabel CRE1

##residues ##molecule_type DNA

SUMMARY FEATURE KEYWORDS CLASSIFICATION Matches Query Match 4.2%; Best Local Similarity 31.8%; 76-262 265-434 156,160,166 ##residues ##molecule_type mRNA 27; \$superfamily MAM homology; astacin homology
hydrolase; metalloprotein; proteinase; zinc #length 748 #molecular-weight 85138 #checksum Conservative #binding_site zinc (His) #status predicted #domain astacin homology #label AST\ 1-748 ##label COR #domain MAM homology #label MAM\ Score 155; DB 12; Length 748; Pred. No. 3.45e-06; 23; Mismatches 31; Indels 31; Indels 4; 2333 Gaps 4.

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REFERENCE REFERENCE ALTERNATE_NAMES ENTRY RESULT ACCESSIONS ORGANISM displays several novel structural domains. #cross-references MUID:89125585 #accession S15447 #title #authors Pfeifer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
journal Cell (1989) 56:291-301
title Functional dissection and sequence of yeast HAP1 activator.
cross-references MUID:89106221 accession **fauthors** journal ##residues ##molecule_type DNA ##cross-references EMBL:J03152 11 CYP1 (HAP1) regulator of oxygen-dependent gene expression yeast. I. Overall organization of the protein sequence Creusot, F.; Verdiere, J.; Gaisne, M.; Slonimski, P.P. J. Mol. Biol. (1988) 204:263-276 A31312 regulatory protein HAP1 - yeast (Saccharomyces cerevisiae) regulatory protein CYP1 30-Sep-1991 *sequence_revision 30-Sep-1991 *text_change S15447 A31312 A31312; S15447; S05804; S15446 formal_name Saccharomyces cerevisiae 13-Sep-1995 1-1483 ##label PFE #type complete Ħ

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Best Local Similarity 31.6%;
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Best Local Similarity 31.6%;
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1388-1483
                                    #authors
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389-394, 415-420
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                                                                                                                                                                                                                               242 EHLALLISSFLEAQASPGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
                                                                                                                                                                                                                                                                                                   184 KFPLTCDGCGKKKIPRETFQDHVRACSKCRV--LCRFHTVGCSEMVETENLQDHELQRLR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL:U20865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 KFPLTCDGCGKKKIPRETFQDHVRACSKCRV--LCRFHTVGCSEMVETENLQDHELQRLR 241
                                                                                                                                                                                                                                                                                                                                 59 riplscticrkrkvkcdklrphcqqctktgvahlchymeqtwaeeaekellkdnelkklr 118
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#length 1483
                                                                                                                                  A47380 #type complete RING finger-containing DNA binding protein RING1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1995 The sequence of S. cerevisiae cosmid 9672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S59400
                                                                                                   #formal_name Homo sapiens #common_name man
21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S59400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S59386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYC1/CYP3 transcription activator - yeast (Saccharomyces
                               Lovering, R.; Hanson, I.M.; Borden, K.L.; Martin, S.;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hength 1502 #molecular-weight 166106 #checksum 7669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            formal_name Saccharomyces cerevisiae
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O'Reilly, N.J.; Evan, G.I.; Rahman, D.; Pappin, Trowsdale, J.; Freemont, P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerevisiae)
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                                                                                         18-Nov-1994
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Pred. No. 6.15e-06;
23; Mismatches 29;
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Pred. No. 6.15e-06;
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                  D.J.;
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ENTRY

A44272

#type complete

ORGANISM

photomorphogenesis repressor COP1 - Arabidopsis thaliana #formal_name Arabidopsis thaliana #common_name mouse-ear

30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change

RESULT ENTRY Ş 밁 Ş 밁 Ъ RESULT SUMMARY FEATURE CLASSIFICATION REFERENCE Ş SUMMARY ACCESSIONS ORGANISM TITLE 3.8%;
Best Local Similarity 32.9%;
Matches 28; Concernation Matches Query Match 3.8%; Score 141; DB 11; Best Local Similarity 32.6%; Pred. No. 1.86e-04; 43-229 232-401 #accession #authors #journal cross-references MUID: 93211912 #title f journal 403 vwtvrnfsqv-len-tskgdklqsprfynse-gygfgvtlypnsress-g-ylrlafhvc 457 :| : :| : | | | | | | | | : :| | : : | | | | | | ##status 415 KGPNDALLQWPF-NQKVTLMLLDHN 458 sgendailewpvenrqviitildqe ##residues ##molecule_type mRNA 355 IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414 ##note ##cross-references NCBIN:128010; NCBIP:128011 ##residues ##molecule_type DNA; protein 13 lhselmcpicldmlkntmttkeclhrfcsdcivtalrsgnkecptc 58 28 LEAKYLCSACKNILRRPFQA-QCGHRYCSFCLTSILSSGPQNCAAC 72 14 5 15; :: - :: :: :: #superfamily MAM homology; astacin homology S39464 sequence extracted from NCBI backbone
#length 377 #molecular-weight 39145 #cheo A47380 FEBS Lett. (1993) 335:367-375 Cloning of the PABA peptide hydrolase alpha subunit S39464 #length 714 #molecular-weight 80703 #checksum S39464 PABA peptide hydrolase alpha chain - human formal name Homo sapiens fcommon name man 19-May-1994 fsequence_revision 17-Nov-1995 Proc. Natl. Acad. Sci. U.S.A. (1993) 90:2112-2116 Dumermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang, Conservative Identification and preliminary characterization of a protein Sterchi, E.E. 01-Dec-1995 motif related to the zinc finger. in COS-1 cells. (PPH-alpha) from human small intestine and 1-377 ##label 1-714 ##label DUM #domain MAM homology #label MAM #domain astacin homology #label AST\ preliminary preliminary #type complete Score 139; DB 11; Pred. No. 3.24e-04; 21; Mismatches 30; 14; Mismatches 16; Indels 438 482 М 30**;** Length 714; Length 377; #checksum Indels #text_change its expression 6; Ξ. 3852 Gaps Gaps **E** 6, :

ACCESSIONS
A44272

REFERENCE
A44272

#authors
Deng, X.W.; Matsui, M.; Wei, N.; Wagner, D.; Chu, A.M.;
Feldmann, K.A.; Quail, P.H.
#journal
Cell (1992) 71:791-801

#title
Doth a zinc-binding motif and a G beta homologous domain.
#cross-references MUID:9304683
#contents
Columbia ecotype
#status
Preliminary; not compared with conceptual translation
#fross-references NCBIP:118657
#frocession
A44272
#frocession
A4

Search completed: Tue Dec 10 07:08:25 1996 Job time : 71 secs.

(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Dec 10 07:06:29 1996; MasPar time 13.19 Seconds 660.452 Million cell updates/sec

Run on:

>US-08-446-915-4 (1-501) from US08446915.pep 3702

Description: Perfect Score:

Sequence: 1 MAAASVTSPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 501

Scoring table: PAM 150 Gap 11

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 50.182; Variance 93.568; scale 0.536

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

13	: =	10	9	&	7	6	Ç	4	ω	1	1	No.	•
120	120	126	135	141	153	157	158	162	229	716	3702	Score	
3.2	3.2	3.4	3.6	3.8	4.1	4.2	4.3	4.4	6.2	26.3	100.0	Query Match	oto
1863	160	647	675	377	1483	668	487	760	458	409	501	Query Match Length DB	
⊢ ∞	9	9	2	-1	2	5	δ	5	2	00	œ	BB	
BRC1_HUMAN	YNN1_CAEEL	ZG48 XENLA	COP1 ARATH	RIN1 HUMAN	CYP1 YEAST	MEPB_RAT	RA18 YEAST	MEPA MOUSE	DG17 DICDI	TRF1 MOUSE	TRF2 MOUSE	ID	
TROPOMYOSIN ALPHA CHA BREAST CANCER TYPE 1	HYPOTHETICAL 18.7 KD	GASTRULA ZINC FINGER	COP1 REGULATORY PROTE	RING1 PROTEIN.	CYP1 ACTIVATORY PROTE	MEPRIN A BETA-SUBUNIT	DNA REPAIR PROTEIN RA	MEPRIN A ALPHA-SUBUNI	DG17 PROTEIN.	THE RECEPTOR ASSOCIAT	TNF RECEPTOR ASSOCIAT	Description	
3.06e-03 2.21e-03	2.21e-03	3.04e-04	1.40e-05	1.69e - 06	2.17e-08	4.90e-09	3.37e-09	7.47e-10	1.30e-21	1.75e-178	0.00e+00	Pred. No.	

45	44	43	42	41	40	39	38	37	36	<u>ა</u> ვ	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
101	101	101	101	101	101	100	101	101	102	102	105	104	105	104	102	104	102	103	104	104	104	107	106	109	106	110	112	111	110	114	113
2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8		2.8	2.8	2.8	2.8	2.9		2.9	2.9	3.0					3.1
1978	1314	465	454	403	337	284	284	284	1959	811	648	624	463	458	430	309	284	284	284	284	248	879	458	393	389	1043	1042	1040	529	501	400
رح.	_	œ	œ	4	9	œ	œ	∞	5	4	~	_	∞	∞	_	5	œ	œ	œ	œ	œ	5	4	υ	5	7	7	~	9	œ	6
MYSG_CHICK	ADR 6_YEAST	VIME HUMAN	TNR1 MOUSE	K1CS MOUSE	ZG26 XENLA	TPMA XENLA	TPMB HUMAN	TPMB RABIT	MYSN_CHICK	HSP7 YEAST	CHA4 YEAST	A33 PLEWA	VIM4 XENLA	VIM1 XENLA	AROA STAAU	MYSA MESAU	TPM1_CIOIN	TPMB CHICK	TPM1 CHICK	TPM1 HUMAN	TPM3 CHICK	MYSP DROME	IF3T TORCA	MLZ4 MOUSE	MYSP SCHJA	RAG1 HUMAN	RAG1 RABIT	RAG1_MOUSE	ZG20 XENLA	UVS 2 NEUCR	OMPA THEMA
MYOSIN HEAVY CHAIN, G	TRANSCRIPTION FACTOR	VIMENTIN.	CROSIS		GASTRULA ZINC FINGER	ALPH	TROPOMYOSIN BETA CHAI		•	MITOCHONDRIAL HEAT SH	CHA4 ACTIVATORY PROTE	ZINC-BINDING PROTEIN	VIMENTIN 4.		3-PHOSPHOSHIKIMATE 1-	MYOSIN HEAVY CHAIN, C	•	TROPOMYOSIN BETA CHAI	TROPOMYOSIN 1, SMOOTH	TROPOMYOSIN ALPHA CHA		PARAMYOSIN, LONG FORM	TYPE III INTERMEDIATE	ZINC FINGER PROTEIN M			V(D) J RECOMBINATION A	V(D) J RECOMBINATION A		PROTEIN.	OUTER MEMBRANE PROTEI
7.64e-01	7.64e-01	7.64e-01	7.64e-01	7.64e-01	7.64e-01	1.02e+00	7.64e-01	7.64e-01	5.73e-01	5.73e-01	2.37e-01	3.19e-01	2.37e-01	3.19e-01	5.73e-01	3.19e-01	5.73e-01	4.28e-01	3.19e-01	3.19e-01	3.19e-01	1.31e-01	1.76e-01	7.12e-02	1.76e-01		2.82e-02		5.24e-02	1.51e-02	2.07e-02

ALI GNMENTS

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Be Qu	QS	Ŧ	Ξ	DR	DR	ឧ	S	S	င္ပ	8	æ	RA	æ	RР	æ	న	റ്റ	8	Æ	ΡŢ	ΡŢ	3	AC	Ħ	RESU
Query Match 100.0%; Score 3702; DB 8; Length 501; Best Local Similarity 100.0%; Pred. No. 0.00e+00;	SQ SEQUENCE 501 AA; 56026 MW; 1264825 CN;	FT ZN_FING 34 72 C3HC4-TYPE.	KW ZINC-FINGER; COILED COIL.	DR PROSITE; PS00518; ZINC FINGER C3HC4.	DR EMBL; L35303; L35303.	CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	CC -!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.	CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.	CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).	CC -:- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN	RL CELL 78:681-692(1994).	RA ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;	RX MEDLINE; 94349371.	RP SEQUENCE FROM N.A.	RN [1]	OC EUTHERIA; RODENTIA.	OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	OS MUS MUSCULUS (MOUSE).	DE THE RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).	DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)		DT 01-FEB-1995 (REL. 31, CREATED)		ID TRF2 MOUSE STANDARD; PRT; 501 AA.	RESULT 1
												\													

Matches

501;

Conservative

0;

Mismatches

<u>;</u>

Indels

0; Gaps

0

9

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RESULT RESULT TO THE ACC PT TO Query 01-FEB-1995 (REL. 31, CRE 01-FEB-1995 (REL. 31, LAS 01-FEB-1995 (REL. 31, LAS TNE RECEPTOR ASSOCIATED F MUS MUSCULUS (MOUSE) P39428; ROTHE T EMBL; TRF1 SEQUENCE FROM N.A., MEDLINE; 94349371. COILED COIL. EUTHERIA; RODENTIA. EUKARYOTA; SEQUENCE ÷ 481 421 421 361 361 301 301 241 241 181 121 481 181 121 Local Similarity 61 2 Match FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR SUBCELLULAR LOCATION: CYTOPLASMIC. SUBUNIT: HETERODIMER OF 2 MOUSE E M., WONG S.C., 78:681-692(1994) eacsrqhrldqdkiealsnkvqqlersiglkdlamadleqkvselevstydgvfiwkisd KNSYVRDDAIFIKAIVDLTGL knsyvrddaifikaivdltgl FTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVMKGPNDA ftrkrqeavagrtpaifspafytsrygykmclrvylngdgtgrgthlslffvvmkgpnda EACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQKVSELEVSTYDGVFIWKISD VCPKFPLTCDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVETENLQDHELQRL vcpkfpltcdgcgkkkipretfqdhvracskcrvlcrfhtvgcsemvetenlqdhelqrl YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE yescheglcpflltecpackglvrlsekehhteqecpkrslscqhcrapcshvdlevhye MAAASVTSPGSLELLQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS L35302; L35302. METAZOA; 409 (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE) Ä STANDARD; 26.3%; 54.0%; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 45464 AND SEQUENCE OF 123-135 AND HENZEL W.J., FACTOR 1 (TRAF1). ¥. 501 501 Pred. Score TRAF1 PRT; 857796 CN; 972; No. 1.75e-178; AND GOEDDEL D.V.; 409 TRAF2. DB æ **8**; Length 409; THE CYTOPLASMIC 390-402 (TNF-R2) DOMAIN 480 420 420 360 360 300 300 240 240 180 180 120 120 60

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Dec 10 06:50 Matches 455 363 395 303 335 243 275 183 sfqrpqsetnvasgcplffplsklqspkhayvkddtmflkcivd 406 leeklrvfanivavlnkeveashlalaasihqsqldrehllslegrvvelqgtlaqkdqv 242 SFQRPVSDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD MADLEQKVSELEVSTYDGVFIWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRV lgklehslrlmeeasfdgtflwkitnvtkrchesvcgrtvslfspafytakygyklclr1 302 LEQKIATFENIVCVLNREVERVAVTAEACSRQHRLDQDKIEALSNKVQQLERSIGLKDLA 334 121; Conservative STANDARD; 61; US-08-446-915-4.rsp PRT; Mismatches 458 A. 41; Indels Ξ. Gaps 454 394

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RESULT
DT O.O.
DT O.O. 01-0CT-1989 01-0CT-1989 01-FEB-1994 DG17 DICDI P11467;
 DEVELOPMENTAL PRÔTEIN; ZINC-FINGER.

 SIMILAR
 25
 67
 TO DRO;

 ZN_FING
 27
 66
 POTENT.

 ZN_FING
 178
 198
 POTENT.

 SEQUENCE
 458
 AA;
 53015
 MW;
 1107.
 SEQUENCE FROM N.A.
MEDLINE; 88142840.
MRISCOLL D.M., WILLIAMS J.G.;
MOL. CELL. BIOL. 7:4482-4489(1987).
-!- THE EXPRESSION OF DG17 PROTEIN IS DEVE-!- INDUCTION: BY CAMP DURING AGGREGATION. PIR; A29361; A29361. DICTYDB; DD02010; ZFAA. EMBL; M18106; M18106. EUMYCETOZOA; EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA; DICTYOSTELIUM DISCOIDEUM (SLIME ZFAA OR DG17. DG17 PROTEIN. (REL. DICTYOSTELIA. . 12, CREATED)
1. 12, LAST SEQUENCE UPD
1. 28, LAST ANNOTATION U POTENTIAL.
MW; 1107348 TO DROSOPHILA SINA POTENTIAL. MOLD) UPDATE) DEVELOPMENTALLY UPDATE) 2 æ 71-108).

밁 Ş 밁 Š 밁 Ş 뮹 Query Match Best Local Matches 250 176 117 135 192 57 79 Match clmverafdkkecc-ciy-s-fneqiveggtncsppdgasvqmqrnlikd-eengckeki 134 TLKEYESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHC-RAPCSHVDL Similarity 64; 6.2%; llarity 24.8%; Conservative Score 229; DB 2; 1 Pred. No. 1.30e-21; 68; Mismatches 103: 103; Length Indels 458 23; Gaps 232 175

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1006:50

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C578L/6, AND C3H/HE; TISSUE=KIDNEY MEDLINE; 92250517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992
01-DEC-1992
01-NOV-1995
                           SIGNAL
PROPEP
                                                                                                                                                                                                                                 -!- SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NON-COVALENT ASSOCIATION OF TWO DISURIDE-LINKED HETERODIMERS; GENETIC FACTORS DETERMINE WHICH OLICOMER(S) WILL BE FORMED (STRAIN-SPECIFIC).
-!- PIM: N-GLYCOSYLATED; AT LEAST 3 OF THE POTENTIAL SITES ARE USED.
-!- TISSUE SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND
  DOMAIN
                                                                                                                                     EMBL; M74897; M74897.
EMBL; M82962; M82962.
                                                                                                                                                                                                                                                                                                                                                                               WOLZ R.L., HARRIS R.B., BOND J.S.;
BIOCHEMISTRY 30:8488-8493(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUMERMUTH E., STERCHI E.E., JIANG W., FLANNERY A.V., BEYNON R.J.;
J. BIOL. CHEM. 266:21381-21385(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P28825;
                                                                                                                                                                METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
-!- SIMILARITY: THE PROTEIN INCLUDES 1 EGF-LIKE REPEAT.
-!- SIMILARITY: CONTAINS A MAM DOMAIN.
                                                                                                                                                                                                          SALIVARY DUCTS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                         ZYMOGEN;
                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91355206.
                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 77-275 FROM N.A. MEDLINE; 92042028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEPRIN A ALPHA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEPA
                                                                       IYDROLASE;
                                                                                    PROSITE; PS00142; ZINC_PROTEASE.
PROSITE; PS00740; MAM.
                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JIANG W., GORBEA C.M., FLANNERY A.V., BEYNON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 kqv--lpkaldicsngyr 319 ::| :: : || |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 QDHELQRL-REH-LALLLSSFLEAQASPGTLNQVGPELLQRCQILEQKIATFENIVCVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOL. CHEM. 267:9185-9193(1992)
                                                                                                                                                                                                                                                                                                                                                   PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                             A40195; A40195.
1IAF; 31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVERVAVTAEACSROHR 308
                                                        SIGNAL;
                                                      METALLOPROTEASE; ZINC; IGNAL; EGF-LIKE DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 24,
(REL. 24,
(REL. 32,
  1
34
78
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
 33
77
760
726
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=KIDNEY;
MEPRIN A ALPHA-SUBUNIT.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                        GLYCOPROTEIN;
3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.J.,
                                                                     TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOND J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRANT G.A.,
                                                                                                                                                                                                                                                                                                                                                                 SUBSTRATES
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 92221691.
BENIT P., CHANET R., F
YEAST 8:147-153(1992).
                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID DISULFID
                                                                                                                                                                                                                        P10862;
JONES J.S., WEBER S., PRAKASH L.;
NUCLEIC ACIDS RES. 16:7119-7131(1988).
-!- FUNCTION: FUNCTIONS WITH DNA REPAIR PROTEIN RAD5 IN ERROR-FREE
                                                                                                                                                                                           01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                   RA18_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
ACT_SITE
                             SEQUENCE FROM N.A. MEDLINE; 88303333.
                                                                   CHANET R., MAGANA-SCHWENCKE
                                                                           SEQUENCE FROM N.A. MEDLINE; 89232745.
                                                                                                YEAST
[2]
                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                          RAD18 OR YCR66W.
                                                                                                                                                                                  DNA REPAIR PROTEIN RAD18.
                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                     EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                 504 sgdndailewpvenrqaimtildqe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RANSME)
                                                                                                                                                                                                                                                                                                                355
                                                                                                                                                                                                                                                                                                                       447 vwtirnisgilentvkgdk-lv-sprfynse-gygvgvtlypngritsnsgllgltfhly 503 : | | ::: ::: | | : : | | | : : : | | | :
                                                                                                                                                                                                                                   5
YEAST
                                                          74:543-547 (1988).
                                                                                                                                                                                                                                                                        KGPNDALLQWPFNQKVTLM-LLDHN
                                                                                                                                                                                                                                                                                                               IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVM 414
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                    727 754
755 760
775 760
776 445
685 725
167 167
1171 171
77 177
38 699
13 708
0 723
1 41
234
234
270
330
426
452
452
546 1
553 P
614
772 T
                                                                                                                                                                                                                                                                                                                                                  4.4%;
ilarity 32.9%;
Conservative
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                FABRE F.,
                                                                                                                                                                                                                                                                                                                                                   Score 162; DB 5; 1
Pred. No. 7.47e-10;
25; Mismatches 28;
                                                                   N., FABRE F.;
                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
T -> A (IN REF.
; 2920193 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC
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CATALYTIC (ASTACIN DOMA
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                            528
                                                                                                                FAYE G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CATALYTIC)
                                                                                                                                                                                                                                   487
                                                                                                                FUKUHARA H.,
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                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                SOR F.;
                                                                                                                                                                                                                                                                                                                                                                        760;
                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                    Gaps
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-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER

POSTREPLICATION DNA REPAIR. RAD5 INCREASES EFFICIENCY OF

RAD18

FUNCTION.

Dec 10 06:50 US-08-446-915-4.rsp

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RESULT TO 101 DT 101 DT
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Best Local Similarity 40.0%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYP1 YEAST
P12351;
01-OCT-1989
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                     VERDIERE J., GAISNE M., GUIARD B., DEFRANOUX N., SLONIMSKI P.P.; J. MOL. BIOL. 204:277-282(1988).
-!- FUNCTION: REGULATION OF OXYGEN DEPENDENT GENE EXPRESSION. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                             -!- SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                        CREUSOT F., VERDIERE J., GAISNE J. MOL. BIOL. 204:263-276(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYP1 ACTIVATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
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                                       -!- CYP1-18 MUTANT ACTIVATE THE EXPRESSION OF CYP3 (ISO-2) WHILE
                                                                                                                                                                   MEDLINE; 89125586.
                                                                                                                                                                                         MUTANT CYP1-18.
                                                                                                                                                                                                                                   CELL 56:291-301(1989)
                                                                                                                                                                                                                                                      PFEIFER K., KIM K.-S.,
                                                                                                                                                                                                                                                                          MEDLINE; 89106221.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 89125585.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYP1 OR HAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 iwhiqmft---q-llggqt-tvysppfyssk-gy-a-fqinl--dltsp-tnvglyfhli 480
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HEME IS AN EFFECTOR MOLECULE FOR CYP1/HAP1. THE REPEAT REGION
                       REDUCING THAT OF CYC1 (ISO-1)
                                                                                   MODULATES THE EXPRESSION OF ISO-1 AND
                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
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12, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
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Pred. No. 4.90e-09;
23; Mismatches 16;
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POTENTIAL.
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ZINC (CATALYTIC)
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                                                                                   ISO-2 CYTOCHROME
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(SEE FT TABLE) MEDIATES HEME INDUCTION BY MASKING THE DNA-BINDING

Dec 10 06:50

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                                                               01-JUN-1994 (REL. 101-JUN-1994 (REL. 101-OCT-1994 (REL. 101-OCT-1994)
                                                                                       006587;
                                                                                                RIN1
                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
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REPEAT
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REPEAT
                                                        RING1 PROTEIN.
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REPEAT
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EMBL; J03152; J03152.
PIR; S05804; RGBYH1.
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
                        EUTHERIA; PRIMATES
                                EUKARYOTA; METAZOA;
                                         HOMO SAPIENS (HUMAN).
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MEDLINE; 93211912.
       SEQUENCE FROM N.A.
                                                                                                                                                119 ervkslektiskvhsspss 137
                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC; METAL-BINDING; REPEAT; HEME.
                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00463; ZN2_CY6_FUNGAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
                                                                                                                                  242
                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLUSTER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN IN THE ABSENCE OF INDUCER.
                                                                                                                                EHLALLISSFLEAQASPCT 260
                                                                                                                                                               KFPLTCDGCGKKKIPRETFQDHVRACSKCRV--LCRFHTVGCSEMVETENLQDHELQRLR 241
                                                                                                                                                                               riplscticrkrkvkcdklrphcqqctktgvahlchymeqtwaeeaekellkdnelkklr 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                      L0002665; HAP1.
                                                                                                 HUMAN
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1151
                               CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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189
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::
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                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                  23;
                                                                                                                                                                                                         Score 153; DB 2; Length 1483; Pred. No. 2.17e-08;
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N
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S -> R (IN CYP1-18 MUTANT).
                                                                                                                                                                                                                                                                                                                                                                                   CONTAINS A [KR]-C-X-[ILV]-D-H MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLN.
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RESULT

RESULT
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Best Local Similarity 31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.8%;
Best Local Similarity 32.6%;
                                                                                                                    ZN_FING
SEQUENCE
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ZN FING 19 58 C3HC4-TYPE.
DOMAIN 176 231 GLY-RICH.
DOMAIN 285 348 GLY-RICH.
DOMAIN 172 175 NUCLEAR LOCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER EMBL; Z14000; Z14000.
PIR; A47380; A47380.
                                                                                                                                               ZINC-FINGER; NUCLEAR PROTEIN; REPEAT.
ZN_FING 52 89 C3HC4-TYPE.
                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                              EMBL; L24437; L24437.

    -!- SUBCELLULAR LOCATION: NUCLEAR.
    -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
    -!- SIMILARITY: BELONES TO THE BETA TRANSDUCIN FAMILY; CONTAINS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; PLANTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COP1 OR FUS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: ACTS AS A REPRESSOR OF PHOTOMORPHOGENESIS IN DARKNESS, AND LIGHT STIMULI ABROGATE THIS SUPPRESSIVE ACTION. COULD FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL 71:791-801(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DENG X.-W., MATSUI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93046683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P28990; 1CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;

    -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 lhselmcpicldmlkntmttkeclhrfcsdcivtalrsgnkecptc 58 | : : |: | : : : | || : : | || : : : ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 LEAKYLCSACKNILRRPFQA-QCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                                                                                                                                                                                                            TRP-ASP DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH COMPONENTS OF THE G PROTEIN SIGNALING PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AS A NEGATIVE TRANSCRIPTIONAL REGULATOR CAPABLE OF DIRECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  و
  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                     PS00518; ZINC_FINGER_C3HC4.
PS00678; G_BETA_REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00518; ZINC_FINGER_C3HC4.
                                                                                                                    675 AA; 76260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=WHOLE SEEDLING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEI N., WAGNER D., CHU A.M., FELDMANN K.A.,
                             Score 135; DB 2;
Pred. No. 1.40e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 141; DB 7;
Pred. No. 1.69e-06;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).; 716288 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-446-915-4.rsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                    2370819 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 377;
                                                        Length 675;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FREEMONT P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'REILLY N.J.,
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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US-08-446-915-4.rsp

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28 LEAKYLCSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC 72

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         3 3 A B
                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ZINC-FINGER; METAL-BINDING; DNA-BINDING; RE | TAN FING | 317 | 339 | C2H2-TYPE. | TAN FING | 345 | 367 | C2H2-TYPE. | TAN FING | 401 | 423 | C2H2-TYPE. | TAN FING | 429 | 451 | C2H2-TYPE. | TAN FING | 429 | 451 | C2H2-TYPE. | TAN FING | 457 | 479 | C2H2-TYPE. | TAN FING | 545 | 507 | C2H2-TYPE. | TAN FING | 513 | 535 | C2H2-TYPE. | TAN FING | 540 | 563 | C2H2-TYPE. | TAN FING | 541 | 563 | C2H2-TYPE. | TAN FING | 541 | 563 | C2H2-TYPE. | TAN FING | 569 | 591 | C2H2-TYPE. | TAN FING | 569 | 591 | C2H2-TYPE. | TAN FING | 569 | 591 | C2H2-TYPE. | TAN FING | 569 | C2H2-TYPE. | TAN FING | 567 | 619 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 625 | 647 | C2H2-TYPE. | TAN FING | 645 | 647 | C2H2-TYPE. | TAN FING | 645 | 647 | C2H2-TYPE. | TAN FING | 645 | 647 | C2H2-TYPE. | TAN FING | 645 | 647 | C2H2-TYPE. | TAN FING | 645 | 647 | C2H2-TYPE. | TAN FING | 645 | 647 | C
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
  01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZG48 XENLA
P18723;
                                                YNN1 CAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00028; ZINC FINGER C2H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P07248; 1ARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-339 FROM N.A.
MEDLINE; 89345612.
KNOCHEL W., POTING A., KOSTER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASTRULA ZINC FINGER PROTEIN XLCGF48.2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOUWMEESTER T., PIELER T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S06573; S06573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; F33282; F33282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M25871; M25871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. MOL. BIOL. 208:639-659(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIETFELD W., EL-BARADI T., MENTZEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90040698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                              425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POETING A., KNOECHEL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 312-647 FROM N.A.
                                                                                                                                                                             153
                                                                                                                                                                                                                                                                                                                            365
                                                                                                                                                                                                                                                                              97
                                                                            11
CAEEL
                                                                                                                                                                                                                gee-pfvcsecgksfaqspqldlhmrihtgek-pfscsdcgkcftqradlnvhrrt 478
                                                                                                                                                                                                                                                                                                                          rnhtgekpfscsecgkcfkwrsllikhhkthtgdksftcadcgkcfkkfsrltehrkcht 424
                                                                                                                                                                        EQECPKRSLSCQHCRAPCSHVDLEVHYEVCPKFPLTCDGCGKKKIPRETFQDHVRA
                                                                                                                                                                                                                                                                         RREVESIPAVCPNDG-C-TWKGTLKEYESCHEGLCPFLLTECPAC-KGLVRLSE-KEHHT 152
                                                                                                                                                                                                                                                                                                                                                                                                    h 3.4%;
Similarity 28.4%;
                                                                                                                                                                                                                                                                                                                                                                               <u>ყ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 AA;
(REL.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
28, CREATED)
28, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 126; DB 9;
Pred. No. 3.04e-04;
                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86:6097-6100(1989)
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2104456 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EL BARADI T., NIETFELD W.,
                                                                            160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIELER T.,
                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 647;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .≖
                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                     01-JUL-1989
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                      TPMS HUMAN
P10469;
01-JUL-1989
                             LIAUTARD J.-P.;

J. MOL. EVOL. 27:228-235 (1988).

- FUNCTION: THE FUNCTION OF TROPOMYOSIN IN SMOOTH MUSCLE AND
MUSCLE CELLS IS NOT CLEAR.

-!- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.

-!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
-!- ALTERNATIVE PRODUCTS: THE VARIOUS TROPOMYOSIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00518; ZINC FINGER C3HC4.
HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z19156; Z19156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 18.7 KD PROTEIN T02C1.1 IN CHROMOSOME III.
                                                                                                                                  COLOTE S., WIDADA J.S., FERRAZ C., BONHOMME F., MARTI J.,
                                                                                                                                                   MEDLINE; 88333013.
                                                                                                                                                                    TISSUE=LIVER;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                    EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                      TPMI OR TMSA
                                                                                                                                                                                                                                                                                      TROPOMYOSIN ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S28290; S28290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T02C1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WORMPEP; T02C1.1; CE00312.
                                                                                                                                                                                                                                                                                                                                                                                                                                       29 EAKYLCSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                     PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AA; 18675 MW; 132007 CN;
                                                                                                                                                                                                                                                                                                       (REL.
                                                                                                                                                                                                                                                                                                                       (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                 11, CREATED)
1. 11, LAST SEQUENCE UPDATE)
2. 32, LAST ANNOTATION UPDATE)
1A CHAIN, SMOOTH MUSCLE (FRAGME)
                                                                                                                                                                                                                                   CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
THE VARIOUS TROPOMYOSIN ISOFORMS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 9;
Pred. No. 2.21e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C3HC4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                       227
                                                                                                                                                                                                                                                                                    (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                THE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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EMBL; X12369; X12369.

PRODUCED BY ALTERNATIVE MRNA SPLICING.

1006:50

US-08-446-915-4.rsp

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PAR RAPERARA RAPERARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                       FUTREAL P.A., LIU Q., SHATTUCK-EIDENS D., COCHRAN C., HARSHMAN TAVTIGIAN S., BENNETT L.M., HAUGEN-STRANO A., SWENSEN J., MIKI EDDINGTON K., MCCLURE M., FRYE C., WEAVER-FELHAUS J., DING W., GHOLAMI Z., SOEDERKVIST P., TERRY L., JHANWAR S., BERCHUK A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAVTIGIAN S., LIU Q., COCHRAN C., BENNETT L.M., DING W., BELL R., ROSENTHAL J., HUSSEY C., TRAN T., MCCLURE M., ERYE C., HATTIER T., PHELPS R., HAUGEN-STRANO A., KATCHER H., YAKUMO K., GHOLAMI Z., SHAFFER D., STONE S., BAYER S., WRAY C., BOCDEN R., DAYANNTH P., WARD J., TONIN P., NAROD S., BRISTOW P.K., NORRIS F.H., HELVERING L., MORRISON P., ROSTECK P., LAI M., BARRETT J.C., LEWIS C., NEUHAUSEN S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P38398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S05585; S05585.

MIM; 191010; 11TH EDITION.

PROSITE; PS00326; TROPOMYOSIN.

MUSCLE PROTEIN; COILED COIL; REPEAT; ALTERNATIVE SPLICING.

NON TER 1 1
                                                                                                                                                                                    CASTILLA L.H.,
                                                                                                                                                                                                                                                                                                             KAMB A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95025896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1994
  FRIEDMAN L.S., OSTERMEYER E.A.,
                                                                                                                           GARBER J.E., BOYD J., LUBIN M.B., DESHANO M.L., BRODY L.C., COLLINS F.S., WEBER B.L.;
                                                                                                                                                                                                                VARIANTS BC GLY-64 AND GLY-1443,
                                                                                                                                                                                                                                                                                                                                   GHOLAMI Z., SOEDERKVIST P., TERRY L., JHANWAR S., BERCHUK A., IGLEHART J.D., MARKS J., BALLINGER D.G., BARRETT J.C., SKOLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CANNON-ALBRIGHT L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIKI Y.,
                                    /ARIANTS BC G-61,
                                                                                               NAT. GENET. 8:387-391(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS LEU-1637; GLU-1708 AND ARG-1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCIENCE 266:66-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 GIKDLAMADLEQKVSELE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 efaersvtkleksiddle 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRCQILEQKIATFENIVCVLNREVERVAVTAEACS-RQHRLDQDKIEALSNKVQQLERSI 328
                                                                                                                                                                                                                                                                              , WISEMAN R.;
266:120-122(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWENSEN J., SHATTUCK-EIDENS D., FUTREAL P.A., HARSHMAN K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95025878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REL. 31, (REL. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                 COUCH F.J., ERDOS M.R., HOSKINS K.F., CALZONE K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
AND VARIANTS R-356; G-1038; N-1040; R-1183 & G-1613. TERMEYER E.A., SZABO C.I., DOWD P., LYNCH E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GODLGAR D., WISEMAN R., KAMB A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND VARIANT ARG-1775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225728 CN;
                                                                                                                                                                                                                   AND VARIANTS ALA-772 AND ASN-1040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1863 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKOLNICK M.H.;
                                                                                                                                                                                                                                                                                                                                      SKOLNICK M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                             OMPA_THI
Q01969;
                                                             ENGEL A.M., CEJKA Z., LUPAS A., LOTTSPEICH F., BAUMEISTER W., EMBO J. 11:4369-4378(1992).

-!- FUNCTION: LINKS THE OUTER MEMBRANE TO THE INNER MEMBRANE. LONG FIBROUS PROTEIN THAT COULD SERVE TO SEPARATE THE TWO MEMBRANES
                                                                                                                                                                                                          01-0CT-1994 (REL. 30, LAST ANNOTATION U OUTER MEMBRANE PROTEIN ALPHA PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
VARIANT
VARIANT
VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
VARIANT
VARIANT
VARIANT
            EMBL; X68276; X68276.
                   -!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: CONTAINS A COPY OF THE S-LAYER HOMOLOGY (SLH) DOMAIN.
                                                                                                                               STRAIN=MSB8 / DSM 3109;
                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                    THERMOTOGA MARITIMA.
PROKARYOTA; NOT YET
                                                                                                                                                                                               OMP-ALPHA.
                                                                                                                                                                                                                                    01-JUL-1993
                                                                                                                                                                                                                                                  01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZN_FING
                                                                                                                   MEDLINE; 93049187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DISEASE: BREAST CANCER (BC) IS AN EXTREMELY COMMON MALIGNANCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAT. GENET. 8:399-404(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROWELL S.E., KING M.-C.;
                                                   -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYMORPHISM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN; DISEASE MUTATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 113705; 11TH EDITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U14680; U14680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00518; ZINC_FINGER_C3HC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

    -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .!- FUNCTION: NOT KNOWN, MAY REGULATE GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                            Match 3.2%;
Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                31 KYL-CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC
                                                                                                                                                                                                                                                                                                                                                     20 kilecpiclelikepvstkcdhifckfcmlkllnqkkgpsqcplc
S28022; S28022
                                                                                                                                                                                                                                                                           THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF INHERITED BREAST AND OVARIAN CANCER (BOC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESPONSIBLE FOR 45% OF INHERITED BREAST CANCER AND MORE THAN 80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONSET BREAST CANCER. MUTATIONS IN BRCA1 ARE THOUGHT TO BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENT OF THE DISEASE, AND THIS LINK IS STRIKING FOR EARLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFFECTING ONE IN EIGHT WOMEN DURING THEIR LIFETIME. A POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1443
1613
1637
1708
1775
                                                                                                                                                                                                                                                  (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1040
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                                                                                                                                                                                                                                    (REL.
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61
64
356
772
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-ONCOGENE.
                                                                                                                                                                                                                                                                            STANDARD;
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30,
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61
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372
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1183
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1637
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                                                                                                                                                                     CLASSIFIED
                                                                                                                                           AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     207720 MW;
                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q -> R.
V -> A.
E -> G.
S -> N.
K -> R.
R -> G (IN BREAST CANCER).
S -> C.
P -> L (IN OVARIAN CANCER).
A -> E (IN BREAST CANCER).
M -> R (IN BREAST CANCER).
                                                                                                                                                                                                                                                                                                                                                                                             Score 120; DB 1;
Pred. No. 2.21e-03;
                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C3HC4-TYPE.

C -> G (IN BREAST CANCER).

C -> G (IN BREAST CANCER).
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     16213725 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 1863;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Job time : 28 secs

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RESULT

RESULT

AC P3

AC P3

AC P3

AC P3

AC P3

AC P3

AC P4

AC P4

AC P4

AC P4

AC P5

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                                                                                                               Query Match 3.1%;
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.1%;
Best Local Similarity 20.6%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01072; SLH DOMAIN.
OUTER MEMBRANE; SIGNAL; COILED
SIGNAL 1 20
CHAIN 21 400 OU
DOMAIN 21 84 SI
DOMAIN 85 379 CO
TRANSMEM 380 400 ME
DOMAIN 208 350 3
REPEAT 251 275 2.
REPEAT 326 350 3.
                                                                                                                                                                                                                              ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=C1-T10-34A; MEDLINE; 93241158. TOMITA H., SOSHI T.
                                                                                                                                                                                                                                         PIR; S34825; S34825.

PROSITE; PS00518; ZINC_FINGER_C3HC4.

PROSITE; PS00518; ZINC_FINGER_C3HC4.

ZINC-FING_S4 71 C34C-TYPE.

ZN_FING_189 209 C2HC-TYPE.

ZN_FING_189 209 C2HC-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UVS-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UVS2 NEUCR STANDARD; PRT; 501 AA. P33288; 01-FEB-1994 (REL. 28, CREATED) 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE) 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                         TOMITA H., SOSHI T., INOUE H.;
MOL. GEN. GENET. 238:225-233(1993).
-!- FUNCTION: MAY BE AN ACTIVATOR THAT FUNCTIONS IN THE TRANSCRIPTION
OF DNA REPAIR GENES.
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; FUNGI; ASCOMYCOTINA; PYRENOMYCETES; SORDARIALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UVS-2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D11458; D11458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUROSPORA CRASSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 ALSNKVQ-QLERSIGLKDLAMADLEQKVSELEVSTYD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 avkeeiemefdkeisInrevvnniglklgnls-rdye 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 ASPGTLNQVGPELLQRCQILEQKIATFENIVCVLNREVERVAVTAEACSRQHRLDQDKIE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                           28 veqafrchvckdfydspmltscnhtfcslcirrclsvds-kcplc 71 : | : | : | : : | : : | : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
LEAKYLCSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                              189 209 C2HC-TYPE.
501 AA; 54830 MW; 1166525 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45310 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COILED COIL; TRANSMEMBRANE; REPEAT.
                                                                                                            Score 114; DB 8; I
Pred. No. 1.51e-02;
11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 6;
Pred. No. 2.07e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLH.
COILED COIL.
MEMBRANE ANCHOR (POTENTIAL).
3 x 25 AA APPROXIMATE REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUTER MEMBRANE PROTEIN ALPHA.
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                                                                                                                 19;
                                                                                                                                                                  Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 400;
                                                                                                                 Indels
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Dec 10 06:50 US-08-446-915-4.rsp

Search completed: Tue Dec 10 07:06:57 1996

****************** (MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Dec 10 07:08:41 1996; MasPar time 10.68 Seconds 446.743 Million cell updates/sec

Run on:

Description: Perfect Score: >US-08-446-915-4 (1-501) from US08446915.pep 3702

Sequence: 1 MAAASVTSPGSLELLQPGFS......NSYVRDDAIFIKAIVDLTGL 501

Scoring table: PAM 150 Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Statistics: Mean 35.625; Variance 156.291; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	BB	ID	Description	Pred. No.
	3700	-	501	15	R90578	Mouse TRAF2.	0.00e+00
2	972		409	25	R90577	Mouse TRAF1.	3.96e-79
ω	131		41	16	R91212		5.64e-02
4	120		1863	16	R91208	BRCA1, breast and ova	3.81e-01
5	120		1863	15	R76641	BRCA1 protein.	3.81e-01
6	111		41	16	R91210	BRCA1 polypeptide zin	1.74e+00
7	99		252	_	P94369	Fusion protein congt.	1.24e+01
80	101		700	15	R89145	Chondroitinase AC.	9.00e+00
9	96	2.6	45	16	R91211	RPT1 zinc finger doma	2.00e+01
10	95		200	10	R53430	Human/rat chimeric ci	2.34e+01
=	95		200	10	R53428	Human/rat chimeric ci	2.34e+01
12	95		300	5	00100	United the section of the section of	3 3/2101

45	44	43	42	41	40	39	38	37	36	ဌ	<u>4</u>	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
90	88	89	88	88	88	88	88	88	88	88	88	88	88	89	88	88	88	94	91	94	94	94	94	92	92	97	96	97	97	97	98	90
2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4		2.4		•	2.4	2.5							2.5					2.6		0.0
3685	775	775	673	200	200	200	200	200	200	200	200	200	200	200	192	187	161	3084	1427	908	870	854	594	462	263	2482	1093	885	816	576	475	000
-	2	ω		14	10	13	7	10	7	ω	11	10	σ	فبيو	6	7	7	2	2	12	12	12	δ	<u>-</u>		14	œ	12	12	12	ω	۰
P90290	P70417	P50121	R06552	R83966	R53425	R70146	R37819	R53432	R34431	R13960	R58303	R53424	R31950	R06234	R32856	R37705	R37707	P94758	R10534	R66053	R66051	R66052	R34936	R05766	R03348	R72826	R42818	R66930	R66931	R66929	R15148	TORICA
_	de	Sequence of a polypep	Human 5-lipoxygenase	Ciliary neurotrophic	Human/rat chimeric ci		Sequence of human cil	Human/rat chimeric ci	Sequence of human cil	CNTF.		Human/rat chimeric ci		Human sciatic nerve c	Sequence of neurotrop	Deltal4 hCNTF.		nce of	Human 160kD mediator		MMDA	Human NMDA receptor s	CENP-B.	Portion of peptide an	VP2 sequence for HRV	Human mitosin.	TMF.			AMML chromosome inv(1	Ro/SSA autoantigen.	vbc_r croise chive riise
	6.92e+01	5.94e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	6.92e+01	5.94e+01	6.92e+01	6.92e+01	6.92e+01	•	•		•	•	2.74e+01	3.74e+01	3.74e+01	1.71e+01	2.00e+01	1.71e+01	1.71e+01	1.71e+01	1.46e+01	7.00et01

ALI GNMENTS

င္ပ	PS	PΤ	PΤ	DR	#	Id	PA	PR	PR	PR	ΡF	PD	ΡN	FT	FT	FT	FT	FH	20	2	至	DΕ	DT	AC	IJ	RESULT
Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)	Claim 8; Page 75-76; 116pp; English.	in mediation of biological activities of TNF and CD40 ligands	Tumour necrosis factor (TNF) receptor-associated factors - involved	N-PSDB; T12262.	WPI; 96-049310/05.	Goeddel DV, Rothe M;	(GETH) GENENTECH INC.	22-MAY-1995; US-446915.	28-OCT-1994; US-331394.	27-MAY-1994; US-250858.	25-MAY-1995; U06639.	07-DEC-1995.	W09533051-A1.	/label= Leucine_zipper_region	Region 275351	/label= TRAF_domain	Domain 272501	Key Location/Qualifiers	Mus musculus.	TNF; CD40.	<pre>TRAF2; tumour necrosis factor receptor associated factor 2;</pre>	Mouse TRAF2.	09-APR-1996 (first entry)	R90578;	R90578 standard; Protein; 501 AA.	LT 1

Dec 10 06.53 US-08-446-915-4 rag 3

Ş 밁 Ş 밁 Ş Ş ð 日 Ş 문 Ş 문 Ş ននន្តន្តន្តន្តន ET ET SKW DE AC S 밁 ₽ 문 문 Query Match 99.9%; Best Local Similarity 99.8%; Matches 09-APR-1996 R90577 standard; R90577; activities. Recombinant TRAF2 is obtd. by expression in host cells of a cDNA clone (T12262) isolated using a yeast two-hybrid assay. It is used to identify inhibitors of activities of TNF-R2, CD40 and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic) Region TRAF1; tumour Mouse TRAF1. Sequence shock and rheumatoid arthritis. (R90578) is a new factor capable of specific association with the intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40, and is involved in the mediation of TNF and CD40 ligand biological /label= Leucine_zipper_region Mus musculus. TNF; CD40. /label= 481 481 421 421 361 301 301 241 241 361 181 181 121 121 61 2 1 maaasvtspgslellqpgfsktllgtrleakylcsacknilrrpfqaqcghrycsfclts. ftrkrqeavagrtpaifspafytsrygykmclrvylngdgtgrgthlslffvvmkgpnda eacsrqhrldqdkiealsnkvqqlersiglkdlamadleqkvselevstydgvfiwkisd vcpkfpltcdgcgkkkipretfqdhvracskcrvlcrfhtvgcsemvetenlqdhelqrl yescheglcpflltecpackglvrlsekehhtegecpkrslscqhcrapcshvdlevhye ilssgpqdcaacvyeglyeegisilesssafpdnaarreveslpavcpndgctwkgtlke KNSYVRDDAIFIKAIVDLTGL knsyvrddaifikaivdltgl 501 FTRKRQEAVAGRTP A I FSP AFYTSRYGYKMCLRVY LNGDGTGRGTHLS LFF VVMKGPNDA EACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQKVSELEVSTYDGVFIWKISD REHLALLLSSFLEAQASPGTLNQVGPELLQRCQILEQKIATFENIVCVLNREVERVAVTA rehlalllssfleaqaspgtlnqvgpellqrcqileqkiatfenivcvlnrevervavta VCPKFPLTCDGCGKKKIPRETFQDHVRACSKCRVLCRFHTVGCSEMVETENLQDHELQRL YESCHEGLCPFLLTECPACKGLVRLSEKEHHTEQECPKRSLSCQHCRAPCSHVDLEVHYE ILSSGPONCAACVYEGLYEEGISILESSSAFPDNAARREVESLPAVCPNDGCTWKGTLKE MAAASVTSPGSLELIQPGFSKTLLGTRLEAKYLCSACKNILRRPFQAQCGHRYCSFCLTS 60 TRAF_domain 183..259 501 Conservative (first entry) necrosis factor receptor associated ξ Location/Qualifiers 180..409 Protein; 409 501 Score 3700; DB 15; Pred. No. 0.00e+00; B Mismatches ç Length Indels 501; 0; Gaps 420 240 120 120 480 480 420 360 360 300 240 180 180 60 0

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Best Local S
Matches 12
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27-MAY-1994; US-250858.
28-OCT-1994; US-331394.
22-MAY-1995; US-446915.
                                                                                                                                                                                                                                                                                                                               of a cDNA clone (T12261) isolated from murine interleukin-2-dependent cytotoxic T-cell line CT6. It is used to identify inhibitors of activities of TNF-R2, CD40 and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic) shock and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis factor (TNF) receptor-associated factors - in mediation of biological activities of TNF and CD40 ligan Claim 8; Page 71-72; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T12261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goeddel DV,
                                                                                                                                                                                                                                                                                                                                                                                               activities. Recombinant TRAF1 is obtd. by expression in host cells
                                                                                                                                                                                                                                                                                                                                                                                                             and is involved in the mediation of TNF and CD40 ligand biologica
                                                                                                                                                                                                                                                                                                                                                                                                                          (R90577) is a new factor capable of specific association with the intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse tumour necrosis factor receptor associated factor 1 (TRAF1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 96-049310/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09533051-A1.
  455
                                                                                                                                                                                                      183 leeklrvfanivavlnkeveashlalaasihqsqldrehllsleqrvvelqqtlaqkdqv 242
                                                             363 sfqrpqsetnvasgcplffplsklqspkhayvkddtmflkcivd
                                                                                                                           335
                                                                                                                                       275 LEQKIATFENIVCVINREVERVAVTAEACSRQHRIDQDKIEALSNKVQQLERSIGIKDIA 334
                                                                                                                                                                                                                                                                   Local Similarity
  SFQRPVSDMNIASGCPLFCPVSKMEA-KNSYVRDDAIFIKAIVD
                                                                                                                          MADLEQKVSELEVSTYDGVF IWKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLRV
                                                                                                                                                                                                                                                    121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                   409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rothe M;
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                26.3%;
                                                                                                                                                                                                                                                   Score
Pred.
61; M
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                   972; DB 15;
No. 3.96e-79;
                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                Length
  497
                                406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligands
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                                                                                                                                                                                                                                                    Gaps
                                                                454
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RESULT 3
ID R91212;
AC R91212;
DT 05-JUN-1996 (first entry)
DE RINI zinc finger domain.
KW RINI; BRCA1; breast cancer; ovary cancer; predisposing gene;
KW susceptibility gene; protein replacement therapy; diagnosis;
KW prognosis.
OS Not specified.
PN W09605307-A2.
PD 22-FEB-1996.
PD 11-AUG-1995; U10203.
PF 11-AUG-1995; U10203.
PF 11-AUG-1994; US-308104.
PR 16-SEP-1994; US-308104.
PR 16-SEP-1994; US-308104.
PR 16-SEP-1994; US-308104.
PR 24-MAR-1995; US-408011.
PR 07-JUN-1995; US-488011.
PR 07-JUN-1995; US-483554.
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07-JUN-1995; US-487002.

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US-08-446-915-4_{J188}

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Best Local Similarity 35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                    12-AUG-1994; US-289221.
02-8EP-1994; US-300266.
16-SEP-1994; US-308104.
29-NOV-1994; US-348824.
24-MAR-1995; US-409305.
07-JUN-1995; US-488011.
07-JUN-1995; US-483554.
07-JUN-1995; US-487002.
Claim 1; Page 117-124; 190pp; English.
The BRCAl polypeptide (R91208) is the product of the human BRCAl
                               prods. for diagnosis, prognosis and therapy of cancers,
breast and ovarian cancers
                                                                                                                                                          (MYRI-)
(UTAH )
(USSH )
                                                                                                                                                                                                                                                                                                                                                                                                         susceptibility gene; protein replacement therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                      BRCA1; breast and ovarian cancer predisposing gene product. BRCA1; breast cancer; ovary cancer; predisposing gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R91208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R91208 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (R91212) a DNA-binding protein that includes a RING-finger motif related to the zinc finger, and RFP1 (R91213) a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A sequence (R91210) near the amino terminus of the human BRCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prods. for diagnosis, prognosis breast and ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human cancer predisposing gene, BRCAl - used to deprods. for diagnosis, prognosis and therapy of cancers, partic.
                                                                                                               Wiseman
                                                                                                                                            Futreal AP,
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                            prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor that is the N-terminal domain of the RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      negative regulator of the interleukin-2 receptor in mouse, RIN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; Page 173; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTAH )
                                                              New isolated human cancer predisposing gene, BRCAl - used to develop
                                                                              N-PSDB; T18310.
                                                                                              WPI; 96-139703/14.
                                                                                                                          Shattuck-Eidens DM,
                                                                                                                                                                                                                                                                                                                                                               WO9605307-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domains, including RPT1 (R91211) a protein that appears to be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide (R91208) shows considerable homology to zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 96-139703/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiseman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Futreal AP,
                                                                                                                                                                                                                                                                                                                                 11-AUG-1995; U10203
                                                                                                                                                                                                                                                                                                                                               22-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MYRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cpicldmlkntmttkeclhrfcsdcivtalrsgnkecptc 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSACKNILRRPFQA-QCGHRYCSFCLTSILSSGPQNCAAC 72
                                                                                                               꺝
                                                                                                                                                   UNIV UTAH RES FOUND.
US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                      MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AA;
                                                                                                                                          Goldgar DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldgar DE, Harshman KD, Kamb A, Miki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r DE, Harshman KD, Kamb A, Miki Y;
Skolnick MH, Swenson J, Tavtigian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 131; DB 16;
Pred. No. 5.64e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRCA1 - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                              partic.
                                                                                                                          ۷V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>;</u>
```

RESULT
ID R9
AC R9
DT 05
DE BE

R91210;

05-JUN-1996 (first entry)

BRCAl polypeptide zinc finger domain. BRCAl; breast cancer; ovary cancer; predisposing gene;

R91210

standard;

Peptide; 41

RESULTING RESULT RESULTING RESULT RESULTING RESULT Š S 밁 88888 밁 Matches Query Match 3.2%; Best Local Similarity 33.3%; Query Match 3.2%; Best Local Similarity 33.3%; Matches a method for gene therapy of breast cancer in a patient by ligating the gene with a promoter capable of inducing gene expression into a virus vector (preferably the Moloney murine leukemia retro virus). Vector expressing BRCA1 is then infused into solid tumours or into The BRCAl gene was isolated from a human cDNA library of an adult female normal breast tissue. The BRCAl protein gene can be used. BRCA1 gene in therapy of breast cancer. Claim 50; Page 91-96; 149pp; English. BRCAl; breast cancer; diagnosis; prognosis; gene therapy. BRCA1 protein. R76641; R76641 standard; Protein; 1863 Sequence drugs. ovarian cancer, can also be produced. genes, associated in humans with a predisposition to breast and gene (T18310). It can be obtd. by insertion of BRCA1 DNA into Sequence protein will result in inhibition morrham treutions. Since the BKCAl gene is a negative growth regulic in human breast cells, in-situ expression of the BRCAL malignant effusions. Since the BRCAl gene is a negative by identifying differentially expressed marker Detection, diagnosis and treatment of pre-invasive breast cancer N-PSDB; Q93027. WPI; 95-269208/35. Thompson ME; Holt JT, 14-JAN-1994; US-182961. 17-JAN-1995; US-373799. 20-JUL-1995. WO9519369-A1. Homo sapiens sapiens. as immunogens for the prodn. of antibodies, or to screen therapeutic vector and expression in host cells; products of mutated BRCA1 (UYVA-) UNIV VANDERBILT. 10-MAR-1996 (first entry) 17-JAN-1995; U00608. 31 KYL-CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC 20 kilecpiclelikepvstkcdhifckfcmlkllnqkkgpsqcplc 31 KYL-CSACKNILRRPFQAQCGHRYCSFCLTSILS--SGPQNCAAC 20 kilecpiclelikepvstkcdhifckfcmlkllnqkkgpsqcplc They can also be used in protein replacement therapy. 15; 15; Jensen RA, Obermiller PS, 1863 AA; 1863 AA; Conservative Conservative --------:-::: ::: Score 120; DB 15; Pred. No. 3.81e-01; 11; Mismatches 16 11; Score 120; DB 16; Pred. No. 3.81e-01; A Mismatches 16; Indels Mismatches 16; Indels of tumour Page DL, BRCA1 polypeptides are used growth. genes, Length 1863; Robinson-Benion CL; Length 1863; 64 72 64 also use Ψ ψ Gaps ef. Gaps 'n 2: 2;

-1

The sequence encodes a molecule which is only 4AAs shorter than mature

Query Match 2.7%; Best Local Similarity 31.9%; Matches 22; Conservative

Score 101; DB 15; Pred. No. 9.00e+00; 17; Mismatches 23;

23; Indels

7.

Gaps

5.

Length 700;

Dec 10 06:53 US-08-446-915-4.rag

믕 Ş 맑 ð Š 문 ននន្តន្តន Query Match Best Local S Matches LT 8 R89145 R89145; purification from F. heparinum cells or by expression of the encoding genes (see T10316 and T10317) in host cells. They chondroitinase B (R89146) are capable of degrading chondroitin sulphate polysaccharides. The enzymes, which have calculated mol.wts. of 7,169 and 53,563, respectively, can be obtd. by 07-JUL-1995; U08560. 08-JUL-1994; US-272247. beta-galactosidase. Recombinant organisms contg. DNA encoding the protein can be used to produce polypeptide which is capable of protecting guinea plus against parasitism from T. colubriformis. Sequence useful as tools in determining the role of chondroitin sulphates Flavobacterium heparinum chondroitinase AC (R89145) and proteins osmotic shock and successive chromatography to fractionate N-PSDB; TIU316.

Purification of chondroitinase AC and chondroitinase B - using Tkalec AL, Zimmer WPI; 96-097624/10. (IBEX-) IBEX TECHNOLOGIES R & D INC. Bennett DC, Fink D, Gu K, Laliber W09601894-A1. Protein chondroitin sulphate. Chondroitinase AC; chondroitinase B; chondroitin lyase; See also P94260, and P94366-P94368. contortus 41 kD protein. The 6 AAs on the N-terminus are derived from therapeutic reagents. Claim 7; Page 30-33; 53pp; English. Peptide Flavobacterium heparinum Chondroitinase AC. 22-APR-1996 (first entry) in modulating cellular events, 25-JAN-1996. /label= Mat /label= Sig_peptide 342 VSELE 221 vdrle 225 283 162 eeelrvvgnnlkslevseekalqredsye-eqirtisarlkeaetraefaersvhklqke 227 VETENLQDHELQ-RLREHLALLLSSFLEAQASPGTLNQVGPEL--LQ-RCQILEQKIATF 282 102 vdvdedrcaeletklreaqallheteskseevarklamveadleraeeraeagenkivel ENIVCVLNREVERVAVTAE-ACSRQHRLDQDKIEALSNKVQQLERSIGLKDLAMADLEQK .. :: standard; Protein; 700 Similarity 29; 346 700 252 AA; Zimmermann J; protein Conservative = = = 24..700 Location/Qualifiers 2.7%; Score 99; DB 1; Le Pred. No. 1.24e+01; 35; Mismatches 55; Laliberte M, A and can also be used to develop Linhardt 55; Length 252 Indels ₽. They are ٠, Gaps 341 161 5;

닭 Ş

281 340 224

mdfnvegrg

289

9

qhgpqlqissygavfitgvlklanyvrdtpyalsteklaifsk-yyrdsy-lka-irgsy 280

QKVSELEVSTYDGVFI---WKISDFTRKRQEAVAGRTPAIFSPAFYTSRYGYKMCLR-VY 395

Ş

INGDGTGRG 404

R91211 standard; Peptide; 45

B

R91211;

RPT1; BRCA1; breast cancer; ovary cancer; predisposing gene;

RPT1 zinc finger domain. 05-JUN-1996 (first entry)

susceptibility gene; protein replacement therapy; diagnosis;

Dec 10 06:53

5

IRESULT RESULT R S Ъ Query Match
Best Local Similarity 35.6%;
Matches 21; Conservative R53428 R53428; Example 1; Page 32; 46pp; English.

Recombinant human and rat CNTF have the same number of amino acids and similar mass (22.7 kD). On reducing SDS-PAGE gels, however, recombinant hCNTF migrates as a protein of mol.wt. 27.5 kD while rat CNTF migrates as expected. The hCNTF also has 4 times lower biological Modified human ciliary neurotrophic factor - having a Modified human ciliary neurotrophic factor - having and Misc_difference 63 Misc_difference 56 Misc difference 53 Misc_difference Chimeric Rattus sp. Chimeric chimeric protein; electrophoretic mobility. receptor binding; enhance; nervous system disorder; treatment; Human ciliary neurotrophic factor; hCNTF; mutant; variant; Human/rat chimeric ciliary neurotrophic factor RPN218. Sequence claimed. CNTF. Human CNTF in which Gln at position 63 is replaced by Arg is an arginine residue at position 63 display the mobility of rat which part of the human CNTF was replaced by the corresp. rat sequence (see R53423-R53432). It was found that all variants with than human CNTF. A series of chimeric proteins was prepared in activity towards chick ciliary ganglion neurons than rat CNTF. The biological activity. WPI; 94-151319/18. Panayotatos N; 08-0CT-1993; U09649. 09-0CT-1992; US-959284. W09409134-A. Misc_difference 67 Misc_difference 53 Chimeric Rattus sp. receptor binding; enhance; nervous system disorder; treatment; Human ciliary neurotrophic Human/rat chimeric ciliary neurotrophic factor RPN222 /note= "Ala is substd. 13-DEC-1994 (first entry) rat CNTF competes for binding to the human or rat receptor better 28-APR-1994. /note= *Leu is substd. /note= /note= "Met is substd. /note= "Thr is substd. (REGE-) REGENERON PHARM INC 224 SEMVETENIQDHELQRLREHLALLLSSFLEAQASPGTLNQVGPELLQRCQILEQKIATF standard; protein; 200 "Ala is substd. by Val" Homo sapiens. Homo sapiens. protein; electrophoretic mobility. 200 A Location/Qualifiers Location/Qualifiers ьy by Met" by Val" by Val Met" Score 95; DB 10;,
Pred. No. 2.34e+01;
u'amatches 21; Indels 4; factor; hCNTF; mutant; variant; ₿

Gaps

4;

282

07-JUN-1995; US-487002. 07-JUN-1995; US-483554.

MYRIAD GENETICS INC.

(MYRI-) (UTAH) (USSH)

Futreal AP,

UNIV UTAH RES FOUND. US DEPT HEALTH & HUMAN SERVICES. AP, Goldgar DE, Harshman KD, Kamb A, Miki Y; k-Eidens DM, Skolnick MH, Swenson J, Tavtigian

SV.

WPI; 96-139703/14. Shattuck-Eidens

Miseman

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02-SEP-1994; US-300266. 116-SEP-1994; US-308104. 29-NOV-1994; US-348824. 24-MAR-1995; US-409305. 07-JUN-1995; US-488011.

11-AUG-1995; U10203. 12-AUG-1994; US-289221.

WO9605307-A2 prognosis.

increase glutamine

recombinant

S 뭉

34

Best Matches Query Match

2.6%;
Local Similarity 38.5%;
Nes 10; Conservation

Pred. Score

DB 16; Length 45; 9;

Mismatches 96; DB 16; I No. 2.00e+01;

Indels

0; Gaps

0

1 cpiclellkepvsadcnhsfcracit 26

CSACKNILRRPFQAQCGHRYCSFCLT 59

== == ==

Sequence oncogene

product. A

(R91212) a DNA-binding protein that includes a RING-finger motif related to the zinc finger, and RFP1 (R91213) a putative transcription factor that is the N-terminal domain of the RET

A sequence (R91210) near the amino terminus of the human BRCA1 polypeptide (R91208) shows considerable homology to zinc finger

Example 8; Page 172; 190pp; English. breast and ovarian cancers

prods. for diagnosis, prognosis and therapy of cancers, partic. New isolated human cancer predisposing gene, BRCAl - used to develop

domains, including RPT1 (R91211) a protein that appears to be a negative regulator of the interleukin-2 receptor in mouse, RIN1

DA C U

R53430;

RESULT

R53430 standard; protein;

200 AA

13-DEC-1994 (first entry)

/note= "Gln is substd. by Arg

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0 cc 10 06:53

biological activity. Example 1; Page 31; 46pp; English.

US-08-446-915-4 rag

밁 Ş 망 Ş Best Query Match 2.6%; Best Local Similarity 35.6%; Matches Query Match Matches LT 13 P91461 rat CNTF competes for binding to the human or rat receptor better than human CNTF. A series of chimeric proteins was prepared in which part of the human CNTF was replaced by the corresp. rat sequence (see R53423-R53432). It was found that all variants with an arginine residue at position 63 display the mobility of rat CNTF. Human CNTF in which Gln at position 63 is replaced by Arg is cDNA was prepd. from L cells (fibroblast tumour) and 2PK3 (B cell lymphoma). Host was pref. E. coli NRIL B-18297. Cysteine residues positions 15, 18, 35, 38, 55, 58, 115 and 118, and histidine residu positions 124 and 127 may be involved in metal finger formation. Positions are given from the methionine (a.a 13 in the sequence g Homo sapiens. W08907652-A. Rpt-1 clone cDNA insert.
Regulatory protein T lymphocyte-1; IL-2 receptor; 09-JAN-1990 P91461; Sequence claimed. migrates as expected. The hCNTF also has 4 times lower biological Recombinant human and rat CNTF have the same number of amino acids and similar mass (22.7 kD). On reducing SDS-PAGE gels, however, recombinant Claim 20; fig 2; 58pp; English. gene expression of interleukin-2 receptor and of human lymphotrophic Regulatory protein T lymphocyte-1 gene and corresp. protein - increase WPI; 89-263719/36. Cantor HI, Patarca R, Freeman GJ; human lymphotrophic retroviruses; metal fingers. 10-MAR-1993 activity towards chick ciliary ganglion neurons than rat CNTF. hCNTF migrates as a protein of mol.wt. 27.5 kD while rat CNTF Sequence See also N90702 11-FEB-1988; US-154758. 10-FEB-1989; U00550. 24-AUG-1989. cetroviruses. (DANA) Dana-Farber Cancer Institute. Match 2.6%; Local Similarity 38.5%; 34 CSACKNILRRPFQAQCGHRYCSFCLT 59 27 cpiclellkepvsadcnhsfcracit 52 :: :: standard; peptide; 365 10; 365 AA; 200 AA; Conservative Conservative (revised) (first entry) <u>:</u> -:: Score 96; DB 1; L Pred. No. 2.00e+01; Score 95; DB 10; Pred. No. 2.34e+01 13; Mismatches 21; Indels A Mismatches Length 365; Length 200; and histidine residues at Indels sequence given). 4; 0 Gaps The Gaps at 0; 4.

RESULT ID R1

R15148 standard; Protein; 475 AA.

Dec 10 06:53 US-08-446-915-4.mg

R15148;

W09117171-A.

4-NOV-1991.

Homo sapiens.

Ro/SSA autoantigen. 14-FEB-1992

(first entry)

Autoantibody; autoantigen; SLE; systemic lupus erythematosus.

RESULT ID R6 AC R6 Ş 밁 Best Matches Query Match 26-JUL-1994; U08530. 29-JUL-1993; US-099869. (UNMI) UNIV TEXAS SYSTEM. Peptide /label= MYH11 AMML chromosome inv(16) product.

AMML; acute myelomonocytic leukemia; chromosome-16; inversion; inv(16); CBF-beta; CBFB gene; transcription factor; myosin; MYH11; with serum from a patient having systemic lupus erythematosus. Two clones were reactive with sera (from a panel of lupus patients) which contd. autoantibodies against 52 kD portein.

Both the cDNA and the protein expressed from it, or portions of it, are useful as diagnostic agents in the identification of patients Novel DNA spanning the pericentric inversion of chromosome for the screening of acute myeloid leukaemia Claim 4; Page 28-30; 78pp; English. Claxton D, Collins FS, WPI; 95-082178/11. R66929 standard; Protein; 576 AA. A cDNA library (from human thymus mRNA) in lambda gtll was screened DNA encoding an Ro-SSA autoantigen - useful for diagnosing auto-immune disorders or presence of auto-antibodies Disclosure; Fig 2; 41pp; English. Frank MB, Itoh K; 07-MAY-1990; US-520270. Key SMMHC. 01-SEP-1995 (first entry) R66929; having autoantibodies and in the identification and analysis of the structural and functional properties of the autoantigen and N-PSDB; Q14798. WPI; 91-353712/48. N-PSDB; Q84588. 09-FEB-1995. WO9504067-A. Homo sapiens. application in immunotherapeutic regimens. Sequence 475 AA; 07-MAY-1991; U03139. 'label≃ eptide (OKLA-) OKLAHOMA MED RES FO 3 / Match 2.6%; Local Similarity 28.2%; 16 CSACKNILRRPFQAQCGHRYCSFCLTSILSSGPQNCAAC cpicldpfvepvsiecghsfcqecisqvgkgggsvcpvc 54
|: | : | :|| |: : | |: | CBFB 11; Conservative 1..164 165..576 Location/Qualifiers Liu P, Score 98; DB 3; Length 475; Pred. No. 1.46e+01; 10; Mismatches Siciliano MJ; 18; 72 Indels 16 -<u>,</u> Gaps for 0

PCR was performed on total cellular RNA from 5 AMML patients having

pericentric inversion of chromosome-16, M4Eo subtype. Sequencing

Dec 10 06:53 US-08-446-91S-4_rag

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showed the inv(16) fusion to comprise a sequence from the CBFB

gene, encoding a novel transcription factor, and the MYH11 gene, encoding smooth muscle myosin heavy chain. In 3 patients, nt 1-492 of the CBFB gene were fused to nt 1921 of MYH11 (shown in

8888888 Q84588; predicted aa sequence in R66929). Probes based on inv(16)

can be used for diagnosis of AMML.

Sequence 576 AA;

Query Match 2.6%; Best Local Similarity 29.6%; Score 97; DB 12; Pred. No. 1.71e+01; Length 576;

Matches 16; Conservative 20; Mismatches 15; Indels ω Gaps μ

Ş 414 erstaqknesarqq-lerqnke-lrsklhemegavkskfkstiaaleakiaqle 465 294 ERVAVTAEACSROHRLDODKIEALSNKVOOLERSIGLK-DLAMADLEOKVSELE 346

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Search completed: Tue Dec 10 07:09:39 1996

Job time : 58 secs.

Dec 10 06:49

(MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Dec 10 07:04:40 1996; MasPar time 9.40 Seconds 414.306 Million cell updates/sec

Run on:

Description: Perfect Score: >US-08-446-915-2 (1-409) from US08446915.pep 2945

Sequence: 1 MASSSAPDENEFQFGCPPAP.....KHAYVKDDTMFLKCIVDTSA 409

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0%
Listing first 45 summaries

81589 seqs, 9523651 residues

Database: a-geneseq24

1:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Statistics: Mean 34.957; Variance 160.267; scale 0.218

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 3 4 4	Score 2945 972 112 113 105	Query Match 100.0 33.0 3.8 3.8 3.6	Length 409 501 870 1427 383	12 6 15 BB	ID R90577 R90578 R90578 R31348 R10534 R10534 R62656	Mouse TRAF1. Mouse TRAF1. Mouse TRAF2. Jaagsiekte retrovirus Human 160kD mediator Petunia Ph6 gene prod SefU2 sequence.	Pred. No. 1.47e-259 7.66e-76 1.77e+00 1.51e+00 1.51e+00 5.43e+00
σ (103	ب د د		5 :	R62757	Seffi? segmence	
7	103	3.5		5	R30429	Major Yo paranecplast	
∞	99	3.4		6	R32698	SSP polypeptide produ	
9	99	3.4		16	R78258	SSP 7.7.7.7.7.7.8.9.8	
10	101	3.4		5	R26173	Part of Major Yo para	
=	101	3.4		15	R69851	Ethylene response (ET	
12	101	3.4		2	B 6 9 8 5 7	7th://	

45	44	43	42	41	40	39	38	37	36	<u>ჯ</u>	<u>ب</u>	$_{3}^{3}$	32	<u>∽</u>	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
88	89	88	88	88	88	88	89	88	88	88	88	88	91	90	92	90	91	92	90	92	92	92	95	95	93	93	93	94	100	101	101	101
						3.0			3.0	3.0	3.0	3.0	3.1	3. 1.		ω 	3.1	3.1	3.1	3.1	3.1	3.1	3.2						3.4	3.4	3.4	3.4
5035	2101	1764	1365	897	885	816	615	435	435	433	239	239	15281	1147	955	648	476	462	394	362	320	235	1618	1618	444	405	405	405	1093	738	738	738
ഗ	œ	_	6	16	12	12	5	2	-	2	2	~	&	œ	11	16	œ	_	16	œ	_	_	11	5	16	11	11		œ	15	15	5
R25450	R47173	P91672	R36780	R92751	R66930	R66931	R74630	P91289	P90992	R08335	R04118	R04117	R44929	R41199	R57365	R94906	R43563	R05766	R94559	R41536	P94366	P94260	R60127	R27205	R86801	R61174	R57498	R57499	R42818	R69850	R69849	R69853
	e of the inr	Primary amino acid se	KRE5.	Murine EGF receptor s	AMML chromosome inv(1	AMML chromosome inv(1	Tomato TGETR1 ethylen	Sequence of a segment	Human CD4 antigen		of Enod2b		T. niveum Cyclosporin	CAI antigen.	K39 polypeptide of Le	RAP-1 radiation prote	recepto	Portion of peptide an	ħ	cokiller	protein of T.	protein	Human nestin protein	Human nestin.	T. thermophilus gamma	Corticosteroid bindin	Human corticosteroid	Human varient cortico	,	response		Ethylene response (ET
7.37e+01	6.35e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	6.35e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	7.37e+01	4.71e+01	5.47e+01	4.06e+01		4.71e+01	4.06e+01	5.47e+01	4.06e+01	4.06e+01	4.06e+01	2.57e+01	2.57e+01	3.49e+01	3.49e+01	3.49e+01	3.00e+01	1.19e+01	1.02e+01	1.02e+01	1.02e+01

ALI GNMENTS

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SS	PT	Ť	×	DR	PI	PA	PR	PR	PR	PF	g	PN	召	Ŧ	H	H	Ŧ	S	즟	줖	E	Ħ	A	Ð	RESULT
Claim 8; Page /1-72; 116pp; English. Mouse tumour necrosis factor receptor associated factor 1 (TRAF1)	s of TNF and CD40 li	Tumour necrosis factor (TNF) receptor-associated factors - involved	N-PSDB; T12261.	WPI; 96-049310/05.	Goeddel DV, Rothe M;	(GETH) GENENTECH INC.	22-MAY-1995; US-446915.	28-OCT-1994; US-331394.	27-MAY-1994; US-250858.	25-MAY-1995; U06639.	07-DEC-1995.	WO9533051-A1.	/label= Leucine_zipper_region	Region 183259	/label= TRAF_domain	Domain 180409	Key Location/Qualifiers	Mus musculus.	TNF; CD40.	<pre>TRAF1; tumour necrosis factor receptor associated factor 1;</pre>	Mouse TRAF1.	09-APR-1996 (first entry)	R90577;	R90577 standard; Protein; 409 AA.	LT 1

Dec 10 06:49 US-08-446-915-2 mg

ននននននននន of endotoxic (septic) shock and rheumatoid arthritis. cytotoxic T-cell line CT6. It is used to identify inhibitors of activities of TNF-R2, CD40 and/or LAP1 oncogene, e.g. for treratment of a cDNA clone (T12261) isolated from murine interleukin-2-dependent activities. Recombinant TRAF1 is obtd. by expression in host cells and is involved in the mediation of TNF and CD40 ligand biological intracellular domain of the type 2 TNF receptor (TNF-R2) (R90577) is a new factor capable of specific association with the Local Match h 100.0%; Similarity 100.0%; 409 Score 2945; DB 15; Pred. No. 1.47e-259; Length and CD40

Ş 밁 Matches masssapdenefqfqcppapcqdpseprvlcctaclsenlrddedricpkcradnlhpvs MASSSAPDENEFQFGCPPAPCQDPSEPRVLCCTACLSENLRDDEDRICPKCRADNLHPVS 409; Conservative <u>.</u>. Mismatches 0 Indels 0 Gaps 6 60 0

Ş 문 13 61 PGSPLTQEKVHSDVAEAEIMCPFAGVGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKEWK pgspltqekvhsdvaeaeimcpfagvgcsfkgspqsmqeheatsqsshlylllavlkewk 120 120

밁 Ş 문 181 121 121 SSPGSNLGSAPMALERNLSELQLQAAVEATGDLEVDCYRAPCCESQEELALQHLVKEKLL sspgsnlgsapmalernlselqlqaaveatgdlevdcyrapccesqeelalqhlvkekll 180 240 180

밁 S 241 181 qvlgklehslrlmeeasfdgtflwkitnvtkrchesvcgrtvslfspafytakygyklcl aqleeklrvfanivavlnkeveashlalaasihqsqldrehllsleqrvvelqqtlaqkd AQLEEKLRVFANI VAVLNKEVEASHLALAAS I HQSQLDREHLLS LEQRVVELQQT LAQKD 300 240

밁 Ş 301 241 rlylngdgsgkkthlslfivimrgeydallpwpfrnkvtfmlldqnnrehaidafrpdls QVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCL 360 300

õ 301 RLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPDLS

S В 361 SASFORPOSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVDTSA 409

ij RESULT R90578; 09-APR-1996 R90578 standard; (first Protein; entry) 501 Æ

Mouse TRAF2. TRAF2; tumour necrosis factor receptor associated factor

Mus musculus. TNF; CD40.

ě)omain 272..501 Location/Qualifiers

Region 07-DEC-1995. WO9533051-A1. /label= Leucine_zipper_region /label= TRAF_domain 275..351

27-MAY-1994; US-250858. 28-OCT-1994; US-331394. 22-MAY-1995; US-446915. (GETH) Ų, GENENTECH INC. Rothe M;

25-MAY-1995; U06639.

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WPI; 96-049310/05.

N-PSDB; T12262.

Tumour necrosis factor (TNF) receptor-associated in mediation of biological activities of TNF and factors - involved CD40 ligands

in mediation of biological activities of Claim 8; Page 75-76; 116pp; English.

Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)

(R90578) is a new factor capable of specific association with

activities. Recombinant TRAF2 is obtd. by expression in host cel of a cDNA clone (T12262) isolated using a yeast two-hybrid assay. It is used to identify inhibitors of activities of TNF-R2, CD40 intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40, and is involved in the mediation of TNF and CD40 ligand biological in host cells

and/or LMP1 oncogene, e.g. for treratment of endotoxic (septic) shock and rheumatoid arthritis.

Sequence 501 AA;

Matches 121; Query Match 33.0%; Best Local Similarity 54.0%; Conservative Score 972; DB 15; Pred. No. 7.66e-76; Mismatches 41; Length Indels 501; 1; Gaps

В 275 leqkiatfenivcvlnrevervavtaeacsrqhrldqdkiealsnkvqqlersiglkdla 334 ;

밁 Ş 183 LEEKLRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQKDQV 242

Ş 335 madleqkvselevstydgvfiwkisdftrkrqsavagrtpaifspafytsrygykmclrv 394 :: ||: : : | :: :|| ||: ||: 394 LGKLEHSLRIMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKLCIRL 302

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밁 363 455 sfqrpvsdmniasgcplfcpvskmea-knsyvrddaifikaivd 497

R31348 standard; R31348; Protein; 870 A

Jaagsiekte retrovirus Pol protein. 18-MAY-1993 (first entry)

JSRV; epithelial carcinoma; ovine; sheep; vaccine;

pulmonary adenomatosa; reverse transcriptase.

Jaagsiekte retrovirus.

FR2676455-A.

20-NOV-1992.

17-MAY-1991; 006060.

17-MAY-1991; FR-006060. (INRM) INSERM INST NAT SANTE & RECH MED.

WPI; 93-020250/03.

New Jaagsiekte Retrovirus and characteristic nucleic acid - also derived proteins, probes and antibodies, useful for in vitro N-PSDB; Q35153.

Claim 25; Page 39-42; 75pp; French. derived proteins, probes and antibodies, diagnosis and in vaccines

adenomatosa in sheep. The complete cDNA sequence of the JSRV genome was prepared from an approx. 8.7kb band of poly-A RNA isolated from JSRV causes epithelial carcinoma in ovine animals, partic. pulmonary adenomatosa in sheep. The complete cDNA sequence of the JSRV genome

IN THE SOLL TO THE SOLL TO THE SOLL TO THE SOLL TO THE SOLUTION TO THE SOLUTIO was prepared from an appears. The semi-purified lung lavage samples from infected sheep. The invention includes the Pol amino acid sequence or any part of it invention includes the Pol amino logical reaction with antibod ant ibodies

directed against JSRV

R31349 and Q35153-Q35155

S S

Sequence See also R31346-7,

870 AA;

wery match 3.8%; Best Local Similarity 24.7%;

Pred. No. 1.77e+00; Score 112; DB 6;

Length 870;

RESULT R62656 standard; Protein; 383 AA

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S 밁 Ş В Query Match 3.6%; Best Local Similarity 27.1%; Matches LT 6 R62757 Petunia Ph gene and constructs containing it — for alteration of vacuolar ph used in the formation of blue flowers
Disclosure; Page 42-44, 62pp; English.
The V26 strain of Petunia was used. Poly A RNA was isolated from total RNA from flower buds and used to generate a cDNA library in a protein involved with regulating anthocyanin synthesis in Maize. Comparison of the pH6 and R(S) sequences over the 54 AA helix-loophelix region detected 57% AA identity. Outside this region only 19% Region Salmonella; Nijjar CS, Ralston EJ; Chuck GS, Vacuolar pH; R62656; WO9425598-A. Salmonella SefU2 sequence. R62757; patterning in Drosophial. In plants, the motif is found in R(S), muscle development, and regulators of segmentation and organ motif include the myc family of oncogenes, regulators of neuron and sequence KKVQDLE (ending at residue 245). Proteins including this the sequence NHVLAER (starting at residue 192) and extending to the sequence comprises a helix-loop-helix structural motif starting with cDNA), the sequence for which is claimed (see Q73000 FT). The AA the left hand side of Ac was used to isolate pPet14-1 (contg. pH6 the vector lambda ZapII (Stratagene). The SstI to BamHI fragment at N-PSDB; Q73000. WPI; 94-341349/42. 27-0CT-1994. WO9423561-A. /label= Helix-loop-helix structural motif
/note= "see also 239..245" Petunia hybrida strain V26. Petunia Ph6 08-JUN-1995 26-APR-1993; 26-APR-1994; 10-NOV-1994. identity was found. Sequence 383 AA; (DNAP) DNA PLANT TECHNOLOGY CORP. 16-APR-1993; US-049282. 15-APR-1994; U04173. (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J. 26-JUN-1995 (first entry) 216 QLDREHLLSLEQRVVELQQTLAQKD 236 ql-rkkvqdlearanqteatlqtkd 259 158 YRAPCCESQEELALQHLVKEKLLAQ-LEEKLRVFANIVAVLNKEVEASHLALAASIH-QS 215 178 frkgcsitgeepsgnhvlaerrrreklnerfiilrslypfvtk-mdkasi-lgdtieyvk 235 standard; Protein; 192 23, Courtney-gutterson N, SefU2; vaccine. gene product. US-054452. IB0207 Conservative pH gene; Petunia. (first entry) 192..198 Location/Qualifiers :: :: Score 105; DB 12; I Pred. No. 5.43e+00; 25; Mismatches 32; 8 240 Dooner 班, --------Keller Length 383 Indels 5; Gaps 5;

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Doran JL,

Kay WW;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                          N-PSDB; Q27387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paraneoplastic cerebellar degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R30429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R30429 standard; Protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The isolated SefU2 protein may be used in a vaccine composition to elicit an immune response to Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fimbrial type proteins.
Disclosure; Fig3A-3B; 95pp; English.
                to determine whether a patient is carrying a tumour expressing Yo.
                                 cerebellar degeneration (PCD). Labelled antibodies to Yo can be used
                                                                            This sequence represents the major Yo paraneoplastic antigen polypeptide, and was deduced from the cDNA sequences of
                                                                                                            Claim 5; Fig 7; 57pp; English.
                                                                                                                                             acid - for treatment
                                                                                                                                                                                          WPI; 92-284676/34.
                                                                                                                                                                                                           Furneaux HM, Posner JB;
                                                                                                                                                                                                                                                                                                                                                     ntemor
                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour cancer; brain; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major Yo paraneoplastic antigen (CDR62) encoded by clones pY1 pY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in animals (e.g. food producing animals) and humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella strains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eliciting an immune response to Salmonella - using attenuated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clouthier SC, Col. WPI; 94-358275/44.
When coupled to a therapeutic agent, these Abs can be used to
                                                               operlapping clones pY2 (Q27387) and pY1. Anti-Yo antibodies may be
                                                                                                                                degeneration
                                                                                                                                                                                                                                                                        06-AUG-1992.
                                                                                                                                                                                                                                                                                          WO9213093-A
                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; Q73062.
                                             detected using labelled Yo to see if a patient has paraneoplastic
                                                                                                                                                                                                                                                        24-JAN-1992; U00620
                                                                                                                                                                                                                                                                                                                    /note= "putative zinc finger"
Domain 52..80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1993
                                                                                                                                                                                                                         (SLOK ) SLOAN KETTERING
                                                                                                                                                                                                                                         25-JAN-1991; US-646292.
                                                                                                                                                                                                                                                                                                    'note= "highly acidic (pI=3.4) activating domain"
                                                                                                                                                                                                                                                                                                                                                                 note= "SPKK site"
                                                                                                                                                                                                                                                                                                                                                                                                note= ""super" leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                                                note= "leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 TKRCHESVCGRTVSLFSPAFYTAKYGYKL-C 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 SIHQSQLDR-EHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFLWKITNV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aefsikaic-rvlqvarnswyvrrqqfrlvc 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                           para-neoplastic antigenic polypeptide and its nucleic
or treatment and diagnosis of para-neoplastic cerebella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                zipper"
122..170
                                                                                                                                                                                                                                                                                                                                                  205..231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector constructs, or compsns. contg.
                                                                                                                                                                                                                         INST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 103; DB 12;
Pred. No. 7.45e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                           para-neoplastic cerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCD; neurological symptoms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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48-446-915-2.Te	
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418-446-915-2.rag	
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Best Local Similarity 26.1%;
                           Best Local Similarity
                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R32698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R32698;
                                                                                 Sequence
                                                                                                   The DNA encoding the heptad may be used to transform plants to increase the content of partic. amino acids such as lysine or methionine in seeds or leaves. See also See also R31979-86 and R32659-705.
                                                                                                                                                                                expressed in vivo in plants to serve as a synthetic seed storage
                                                                                                                                                                                                                                                                                                                                                                              09-AUG-1991; US-743006.
                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1992; U06412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heptad;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSP polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activating domain between residues 52 and 80. The leucine zipper was found to have an unusual almost perfect homology with that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete register with that at 171-192. However the characteristic basic DNA binding domain found in many leucine zipper proteins. There are also two other putative DNA binding motifs - a SPKK site at 201 and a zinc finger at 205-231, adjacent to the leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secondary structure analysis of this sequence reveals a highly hydrophilic protein with extensive regions of alpha helix. There
                                                                                                                                                             protein which can be custom-tailored for specific end-user requirements.
                                                                                                                                                                                                  The sequence represents a synthetic heptad polypeptide which can
                                                                                                                                                                                                                      Disclosure; Page 130; 176pp; English.
                                                                                                                                                                                                                                           proteins with specified aminoacid content
                                                                                                                                                                                                                                                            expressed in vivo in plants to serve as custom-tailored storage
                                                                                                                                                                                                                                                                                Synthetic polypeptide(s) contg. specified heptad units
                                                                                                                                                                                                                                                                                                    N-PSDB; Q37279.
                                                                                                                                                                                                                                                                                                                        WPI; 93-076517/09.
                                                                                                                                                                                                                                                                                                                                        Falco SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9303160-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor is the presence of a highly acidic (pI=3.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zipper. Also consistent with the proteins function as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser164 and His137 a "super" leucine zipper stretches from 122-170 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at residues 171-192. In addition allowing the substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also a leucine zipper motif, distinctive of DNA binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and when coupled to an imaging agent to locate neoplastic cells.
                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found in C-Fos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibit proliferation of neoplastic cells in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 vyeql-dvtareleetnqklvadskasq-qk--ilsltetieclqtnidhlqsqv 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 LERNIS-ELQI-QAAVEATGDLEVDCYRAPCCESQEEL-ALQHLVKE-KLLAQI-EEKLR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 VFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQ-KDQV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 lqqdlqlaaelgktlldrntele-dsvqqmyttnqeqlqeieyltkqvellrqmneqhak 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plants;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                 77 AA;
                                                                                                                                                                                                                                                                                                                                        Keeler SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           custom tailored storage proteins; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produced from clone 2-9.
                         24.3%;
                                                                                                                                                                                                                                                                                                                                            Rice
     Pred.
22; N
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Pred. No. 7.45e+00;
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ie 99; us ., .d. No. 1.39e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::
                                         Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 11;
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/label=
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SSP 7.7.7.7.7.8.9.8.9.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R78258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R78258 standard; Protein; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                  Lysine-rich synthetic storage protein SSP 7.7.7.7.7.7.8.9.8.9.5. (R78258) comprises 6 heptad SSP7 repeats (see R78237) followed by alternating SSP8 (R78245) and SSP9 (R78246) heptads and a C-terminal SSP5 heptad (R78236) derived from vector pSK6. The SC
                                                                                                                                            chloroplast transport sequence and seed specific promoter, also new
                                                                                                                                                                                                                              21-NOV-1994; U13190.
30-NOV-1993; US-160117.
17-JUN-1994; US-261661.
                                                                                                                                                                                                                                                                  08-JUN-1995
                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soybean; Glycine max; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dihydrodipicolinic acid synthase; corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lysine; synthetic storage protein; SSP; vector; pSK6;
          be expressed in the seeds of transformed plants to increase the
                      clone 2-9 (Q95004).
                                                                                                                    Example 8; Page 145; 180pp; English.
                                                                                                                               plants of improved nutritional value.
                                                                                                                                                                New chimeric gene providing increased lysine content in plant seeds
                                                                                                                                                                                                        Falco SC,
                                                                                                                                                                                                                                                                                W09515392-A1
                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                               the resulting vector to transform Escherichia coli JM103, yielding
                                            (Q95002-03) into the EarI site of clone 82-4 (Q94992) and use of
                                                         was obtd. by insertion of SSP8.9.8.9-encoding oligonucleotides
                                                                                                                                                                                N-PSDB; Q95004.
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                                                                                                                                                                                                                                                                                             SSPS
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                    The SSP forms a coiled-coil structure.
                                                                                                                                                                                                       Rice
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                                                                     SSP
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BBBBB

Ethylene response (ETR) mutant protein etr1-2.

20-MAR-1996 (first entry)

R69851;

standard; Protein; 738

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RESULT Ş В Ş 밁 Š 밁 맑 Š Query Match Best Local S Matches Matches Best Local Similarity 24.3%; Query Match R26173 R26173; When coupled to a therapeutic agent, these Abs can be used to inhibit proliferation of neoplastic cells in a patient with PC detected using labelled Yo to see if a patient has paraneoplastic cerebellar degeneration (PCD). Labelled antibodies to Yo can be used WPI; 92-284676/34. N-PSDB; Q27387. Part of Major Yo paraneoplastic antigen (CDR62) encoded by clone pY paraneoplastic cerebellar degeneration; PCD; neurological symptoms; Sequence and when coupled to an imaging agent to locate neoplastic cells Sequence $430~\mathrm{AA};$ to determine whether a patient is carrying a tumour expressing Yo. clone pY2 as detailed in Q27387. Anti-Yo antibodies may be This sequence represents part of the major Yo paraneoplastic antigen polypeptide, and was deduced from the cDNA sequence of Claim 5; Fig 7; 57pp; English. degeneration acid - for treatment and Major Yo para-neoplastic Furneaux HM, Posner JB; 24-JAN-1992; U00620. 25-JAN-1991; US-646292. 06-AUG-1992. W09213093-A. Homo sapiens. tumour cancer; 27-JAN-1993 (SLOK) SLOAN KETTERING 183 LEEKLRVFANTVAVINKEVEASHLALAASTHQ-SQLDREHLLSLEQRVVELQQTLAQKDQ 241 130 242 VLGKLEHSLRLMEE 187 LRVFANIVAVLNKEVEASHLALAASIHQSQLDREHLLSLEQRVVELQQTLAQ-KDQV 58 akvyeql-dvtareleetnqklvadskasq-qk--ilsltetieclqtnidhlqsqv 110 Local Similarity mes 31; Conser 60 klkkmeeklkwmee 1 meeklkameeklkameeklkameeklkame-eklkameeklkkmeeklkwmee APMALERNISEIQIQAAVEATGDIEVDCYRAPCCESQEEL-AIQHIVKE-KILAQI-EEK 186 standard; Protein; 430 18; 77 3.4%; ilarity 26.5%; Conservative Conservative .. (first entry) A brain; therapeutic agent; imaging; ss. 255 73 INST CANCER antigenic polypeptide and its nucleic diagnosis of para-neoplastic cerebellar Score 101; DB 5; I Pred. No. 1.02e+01; 29; Mismatches 46; Pred. Score 22; Mismatches Ä e 99; DB 16; . No. 1.39e+01; 46; 32; Length 430; Length Indels Indels 11; 2; PCD ef. Gaps Gaps 59 10; 2

Dec

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controlled fruit ripening

and delayed floral senescence

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Best Local Similarity 26.8%;
              etr1-3 and etr1-4 respectively. The cDNA sequences which encode these proteins can be linked to a promoter and used to transform plant cells of fruit bearing plants (in partic, the fruit is a
                                                                                        Claim 2; Page 76-80; 212pp; English. R69850-R69853 represent the amino acid sequences of the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                            Ethylene response; recombinant; mutation; decrease; fruit ripening; abscission; floral senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        R69852;
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                                                                                                                                                                      N-PSDB; Q85560.
                                                                                                                                                                                                             Bleecker AB,
                                                                                                                                                                                                                                                                                                                          W09501439-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thaliana mutated ethylene response (ETR) proteins etr1-1, etr1-2, etr1-3 and etr1-4 respectively. The cDNA sequences which encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 71-74; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transformed plants with decrease in response to ethylene
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28-JUN-1994; US-263480.
                                                                                                                                                   Modified ethylene response (ETR) nucleic acid - useful for producing
                                                                                                                                                                                                        (CALY ) CALIFORNIA INST OF TECHN.
Bleecker AB, Chang C, Meyerowit
                                                                                                                                                                                                                                                 28-JUN-1994; US-263480.
                                                                                                                                                                                                                                                                                   30-JUN-1994; U07418.
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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                                                                     thaliana mutated ethylene response (ETR) proteins etr1-1, etr1-2,
                                                                                                                                 transformed plants with decrease in response to ethylene
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resulting
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a decrease in response to ethylene. This enables
                                                                                                                                                                                                          Meyerowitz EM;
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Pred. No. 1.02e+01
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                                                                                                                                                                Query Match 3.4%;
Best Local Similarity 26.8%;
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Best Local Similarity 26.8%;
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01-JUL-1993; US-086555.
28-JUN-1994; US-263480.
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                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                            controlled fruit ripening and delayed floral senescence and
                                                                                                                                                                                                                                                                                             plant cells of fruit bearing plants (in partic, the fruit is a
                                                                                                                                                                                                                                                                                                                                    etrl-3 and etr1-4 respectively. The cDNA sequences which encode
                                                                                                                                                                                                                                                                                                                                                                       transformed plants with decrease in response to ethylene Claim 2; Page 82-86; 212pp; English. R69850-R69853 represent the amino acid sequences of the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bleecker AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abscission; floral senescence.
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                                                                                                                                                                                                                                                                              tomato) resulting in a decrease in response to ethylene. This enables
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224 SLEQ--RVVELQQTLAQKDQVLGKLEH-SLRLMEEASFD-GTFLWKITNVTK 271
                                 381 mvetilkssnllatlmndvldlsrledgslql-elgtfnlhtlfrevlnlik 431
                                                                                        321 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiialssllqeteltpeqr1 380 :| ::: | | ; | ; | ; | ; | ; | ; | ; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-JAN-1995.
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                                                                       ELALQHLVKEKLLAQLEEK-LRVFANIVAVLNKEVEAS-H--LALAASIHQSQLDREHLL 223
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                                                                                                                                                                                                                        during growth, transport or storage. 738 AA;
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyerowitz EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport or storage.
                                                                                                                                                                Score 101; DB 15;
Pred. No. 1.02e+01;
                                                                                                                                                36;
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Pred. No. 1.02e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Mismatches 37; Indels 9;
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RESULT

ET 14 R69849 standard; Protein; 738

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DA CO

R69849;

20-MAR-1996 (first entry)

Ethylene response (ETR) gene product.

abscission; floral senescence.

Ethylene response; recombinant; mutation; decrease; fruit ripening;

WO9501439-A2. Arabidopsis thaliana.

30-JUN-1994; U07418. .2-JAN-1995.

US-08-446-915-2.mg

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S 밁 S ₽ Matches Best Query Match ethylene response (ETR) gene which codes for the ethylene response protein (R69849). The ETR cDNA or the full gene sequence (Q85556) can be mutated and linked to a promoter and used to transform plant cells of fruit bearing plants (in partic. the fruit is a tomato) transformed plants with decrease in response to ethylene Claim 2; Page 65-68; 212pp; English. R69850-R69853 represent the amino acid sequences of the Arabidopsis abscission; floral senescence. Arabidopsis thaliana. Ethylene response (ETR) mutant protein etr1-1. Ethylene response; recombinant; mutation; decrease; fruit ripening; R69850; R69850 standard; Protein; 738 AA. resulting in a decrease in response to ethylene. This enables controlled fruit ripening and delayed floral senescence and transformed plants with decrease in response to ethylene Claim 1; Page 59-62; 212pp; English. N-PSDB; Q85557. Bleecker AB, Chang C, Modified ethylene response (ETR) nucleic acid - useful for producing Bleecker AB, Q85557 represents the cDNA sequence of the Arabidopsis thaliana Modified ethylene response (ETR) nucleic acid - useful for producing WPI; 95-061003/08. thaliana mutated ethylene response (ETR) proteins etri-1, etri-2, etri-3 and etri-4 respectively. The cDNA sequences which encode WPI; 95-061003/08. WO9501439-A2. 01-JUL-1993; plant cells of fruit bearing plants (in partic. the fruit is a these proteins can be linked to a promoter and used to transform 28-JUN-1994; US-263480. 01-JUL-1993; 30-JUN-1994; U07418 20-MAR-1996 (first entry) abscission 28-JUN-1994; US-263480. (CALY) CALIFORNIA INST OF TECHN. 321 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiialssllqeteltpeqrl 380 (CALY) CALIFORNIA INST OF TECHN. 224 SLEQ--RVVELQQTLAQKDQVLGKLEH-SLRLMEEASFD-GTFLWKITNVTK 271 381 mvetilkssnllatlmndvldlsrledgslql-elgtfnlhtlfrevlnlik 431 168 Match 3.4%; Local Similarity 26.8%; ELALQHLVKEKLLAQLEEK-LRVFANIVAVLNKEVEAS-H--LALAASIHQSQLDREHLL 223 30**;** Q85558. during growth, transport or storage. 738 AA; US-086555. Conservative US-086555. Chang C, Meyerowitz EM; Meyerowitz EM; Score 101; DB 15; L Pred. No. 1.02e+01; 36; Mismatches 37; Length 738; Indels 9 Gaps

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tomato) resulting in a decrease in response to ethylene.
   This enables
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- controlled fruit ripening and delayed floral senescence and
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Best Local Similarity 26.8%;
Matches 30; Conservative
        36;
                  Score 101; DB 15;
Pred. No. 1.02e+01;
        Mismatches
                            Length 738;
       Indels 9;
       Gaps
       7;
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- 168 ELALQHLVKEKLLAQLEEK-LRVFANIVAVLNKEVEAS-H--LALAASIHQSQLDREHLL 223 321 dllmeqnvaldlarreaetairarndflavmnhemrtpmhaiialssllqeteltpeqrl 380 :: = :: :: --
- 묽 381 mvetilkssnllatlmndvldlsrledgslql-elgtfnlhtlfrevlnlik 431
- 224 SLEQ--RVVELQQTLAQKDQVLGKLEH-SLRLMEEASFD-GTFLWKITNVTK 271

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